

FIGURE 1A

20CAGHA

CTGCAGGCCAGCGTCCTGATAAGTGAATTGCGCCGCCACCATGGGAGGCCCCAC
CGTCAACCCCCCAGCAGCAGCAACAGCAGCAGCAACAGCAACAGCAGCAGC
AACAACAGCAGCAGCAACAGACTAGTCGTACGTATCCCTATGACGTGCCCGA
CTATGCGTAG

127CAGHA

CTGCAGGCCAGCGTCCTGATAAGTGAATTGCGCCGCCACCATGGGAGGCCCCAC
CGTCAACCCCCCAGCAGCAGCAACAGCAGCAGCAACAGCAACAGCAGCAGC
AACAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAAC
AGCAACAGCAGCAGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAAC
AGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAACAGCAACAGCAAC
AGCAGCAGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAGC
AGCAACAGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAGC
AGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAGCAGCTGCAAC
AGCAACAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACAGCAACAGCAAC
CCTATGACGTGCCCGACTATGCGTAG

FIGURE 1B

20QHA

MGGPPSTPQ₂₀*TSRTYPYDV*PDYA

127QHA

MGGPPSTPQ₁₂₇*TSRTYPYDV*PDYA

Figure 1. A) DNA sequences of 20QHA and 127QHA and B) their predicted protein sequences. The protein-coding region is underlined. The Kozak sequence is in italic.

FIGURE 2

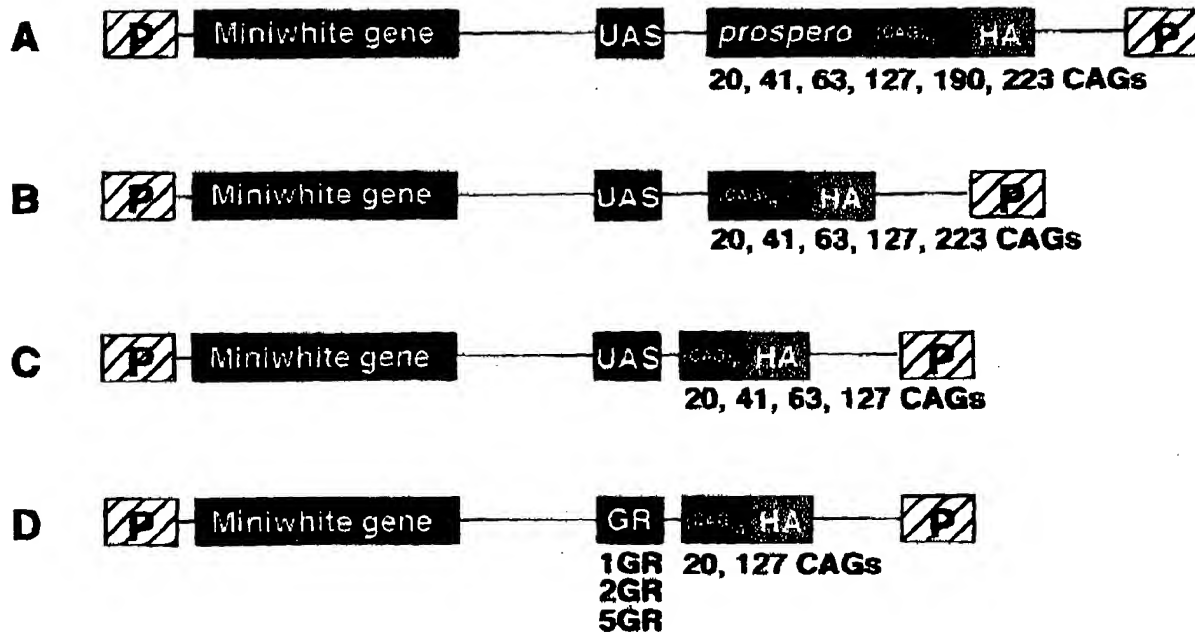


Figure 1. P-element plasmid constructs for production of transgenic flies. Each construct has two P-elements for chromosomal insertion. To facilitate identification of transformed flies, a miniwhite gene is included to produce red pigmentation in the eye. **A)** Plasmids carrying the full-length cDNA encoding the fly PROSPERO with various CAG repeat sizes. The expression of PROSPERO is regulated by five tandem upstream activating sequences (UAS). The yeast transcription factor GAL4 activates the transcription from these UAS elements. At its 3'-end, *prospero* cDNA is joined, in-frame, to a short DNA sequence that codes for a heterologous epitope, hemeagglutinin (HA). Antibodies against HA will be used to label the protein in immunohistochemical assays and Western blots. **B)** Plasmids carrying a partial cDNA encoding 422 amino acids of the C-terminal end of PROSPERO with various CAG repeat sizes. **C)** Plasmids carrying a DNA sequence that only encodes polyglutamines of various sizes. **D)** Plasmids carrying a DNA sequence that only encodes polyglutamines of various sizes, expressed under the control of one, two or five GLASS response elements (1GR, 2GR, or 5GR). The eye-specific protein GLASS activates the expression of polyglutamines from the GLASS response elements.

FIGURE 3

Generation of the P-element insertion and screening for modifiers

M P[Δ2-3]/P[Δ2-3] **X** **F** EP55/EP55

↓

M EP55/Y;; P[Δ2-3]/+ **X** **F** w/w

↓

M w/Y;pEP/+;+ **or** w/Y;+;pEP/+ **X** **F** w;GMR/CyO;127Q/127Q

↓

Progeny screened for eye phenotype

Isolation of the new P-element insertion (pEP = suppressor or enhancer)

M (GMR;127Q)/pEP **X** **F** (CyO;TM3)/Xa

↓

M GMR/CyO;pEP/TM3 **X** **F** w¹¹¹⁸

↓

M GMR;TM3 **or** CyO;pEP **X** **F** w;GMR/CyO;127Q/127Q to test

X **F** (CyO;TM3)/Xa to establish line

↓

M +/CyO;pEP/TM3 **X** **F** +/CyO;pEP/TM3

↓

pEP/TM3 **or** pEP/pEP established lines

Genetic scheme used for generating P-element mutants, screening for modifiers of polyglutamine toxicity, and isolating a hypothetical modifier P-element insertion on chromosome 3. Homozygous EP55 virgin females were crossed with males homozygous for a defective transposon, expressing the transposase. The F1 male progeny were crossed with virgin w¹¹¹⁸ females. The F2 Male progeny that had coloured eyes and lacked the transposon's genetic markers were selected, as they contain a new stable insertion on an autosomal chromosome. These males were crossed with flies heterozygous for GMR-GAL4 on chromosome 2, balanced by CyO chromosome, and homozygous for UAS-127Q on chromosome 3. The resulting F3 progeny were screened for eye phenotype. Once a modifier was found, a single male was crossed to female (CyO;TM3)/Xa. The resulting male progeny were crossed to w¹¹¹⁸ flies to separate the P-elements. This resulted in colored-eye progeny that carry a balancer for one chromosome and a P-element on another. Males from such progeny were tested for modifier activity by crossing to female w;GMR/CyO;127Q/127Q. The lines were established by crossing the latter males to (CyO;TM3)/Xa, and by crossing the resulting flies carrying CyO and TM3 balancers. **EP55**: source of transposable P-element; **P[Δ2-3]**: source of transposase; **F**: female; **M**: male; **CyO**: balancer chromosome 2; **TM3**: balancer chromosome 3. **Xa**: translocation (2;3) Xa. (Chromosome 4 is omitted.)

Genetic scheme used for generating P-element mutants, screening for modifiers of polyglutamine toxicity, and isolating a hypothetical modifier P-element insertion on chromosome 3.

FIGURE 4

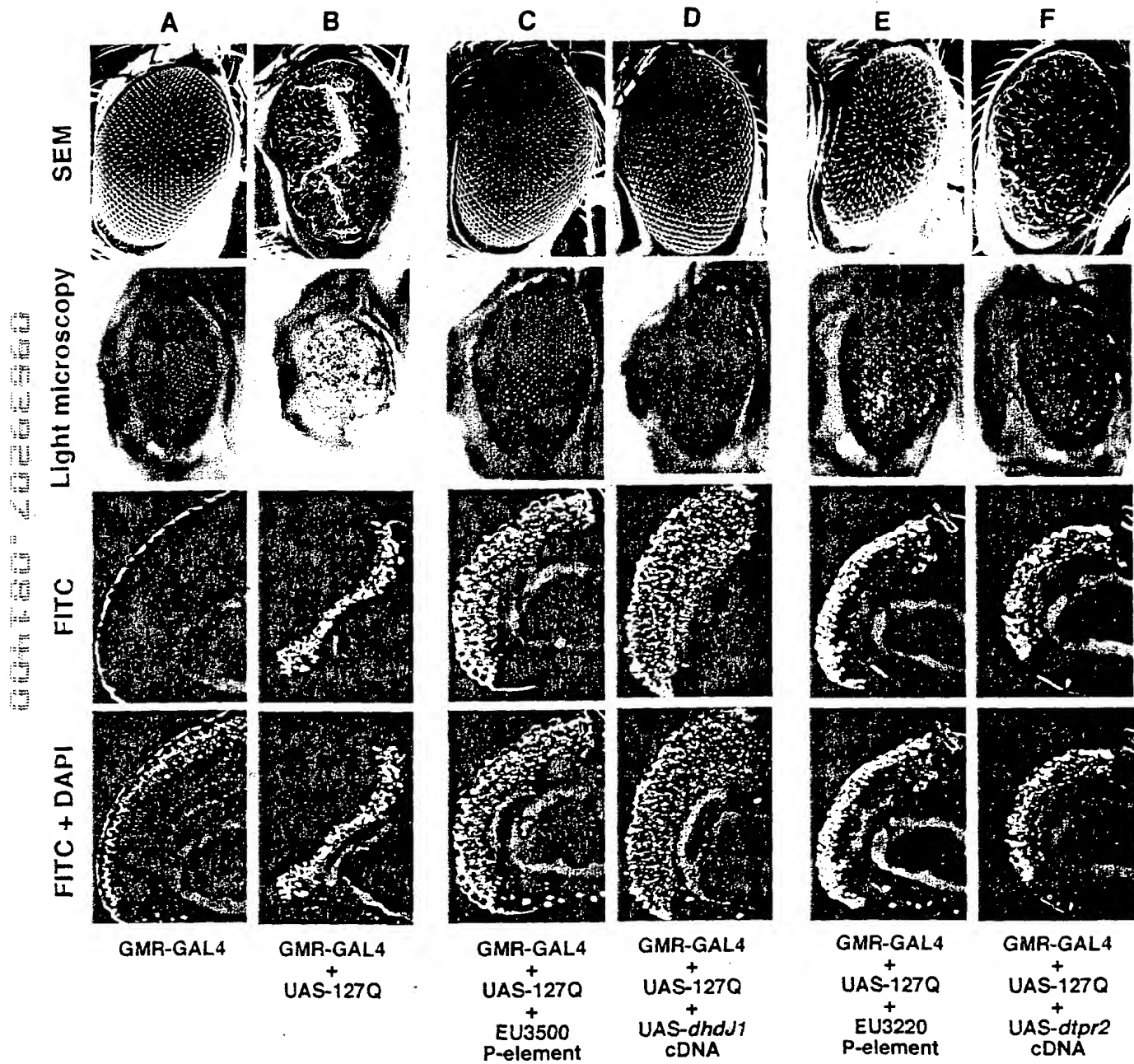


FIGURE 5

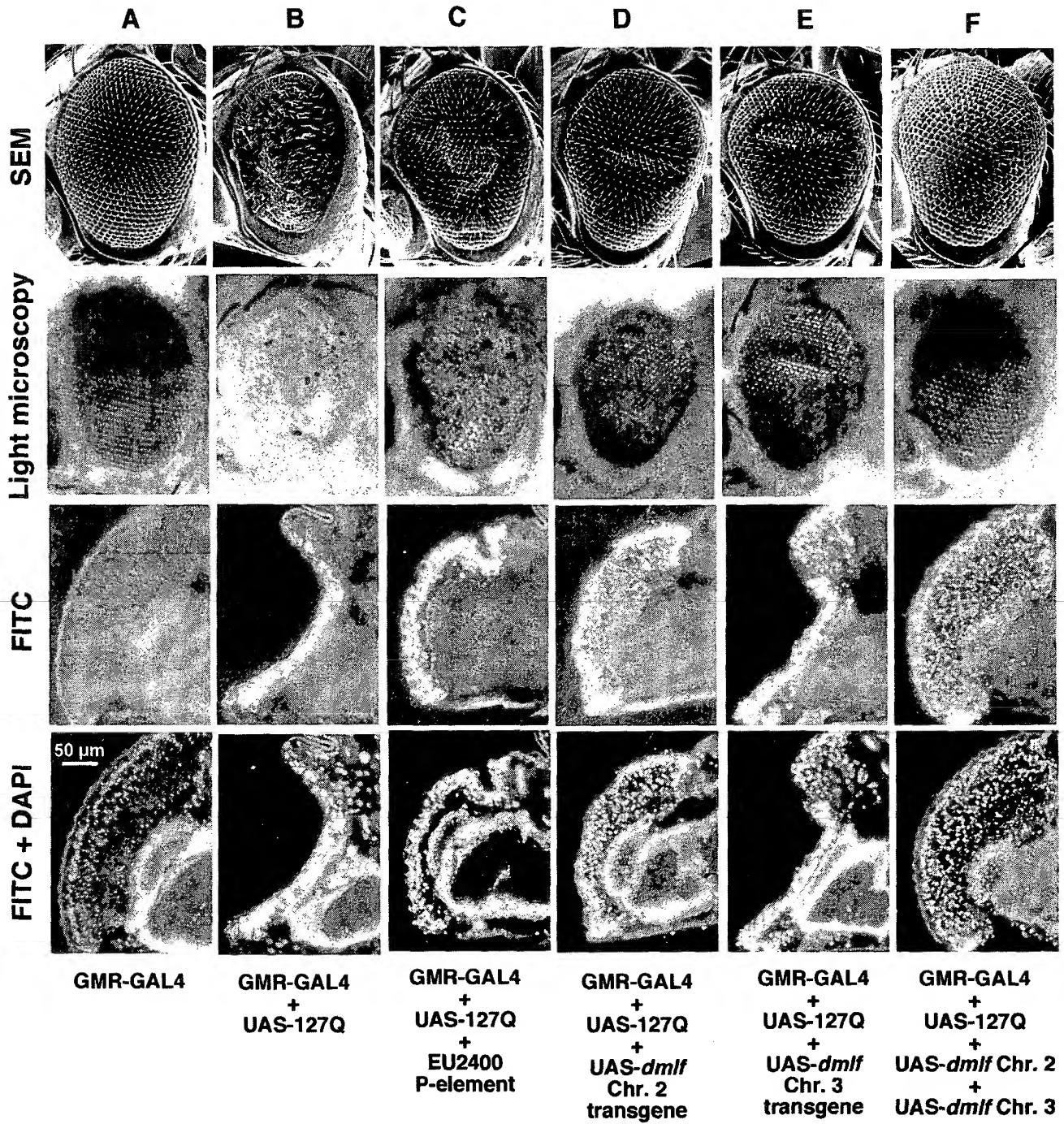


FIGURE 6

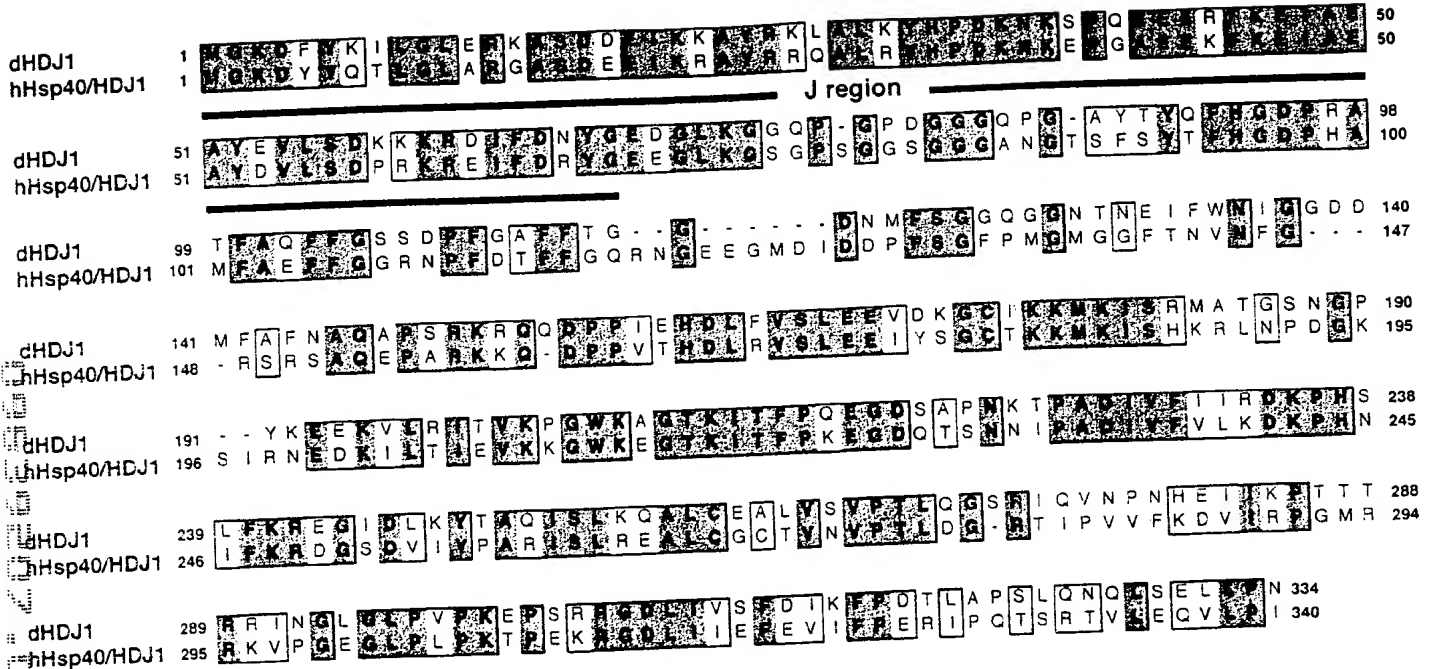


FIGURE 7

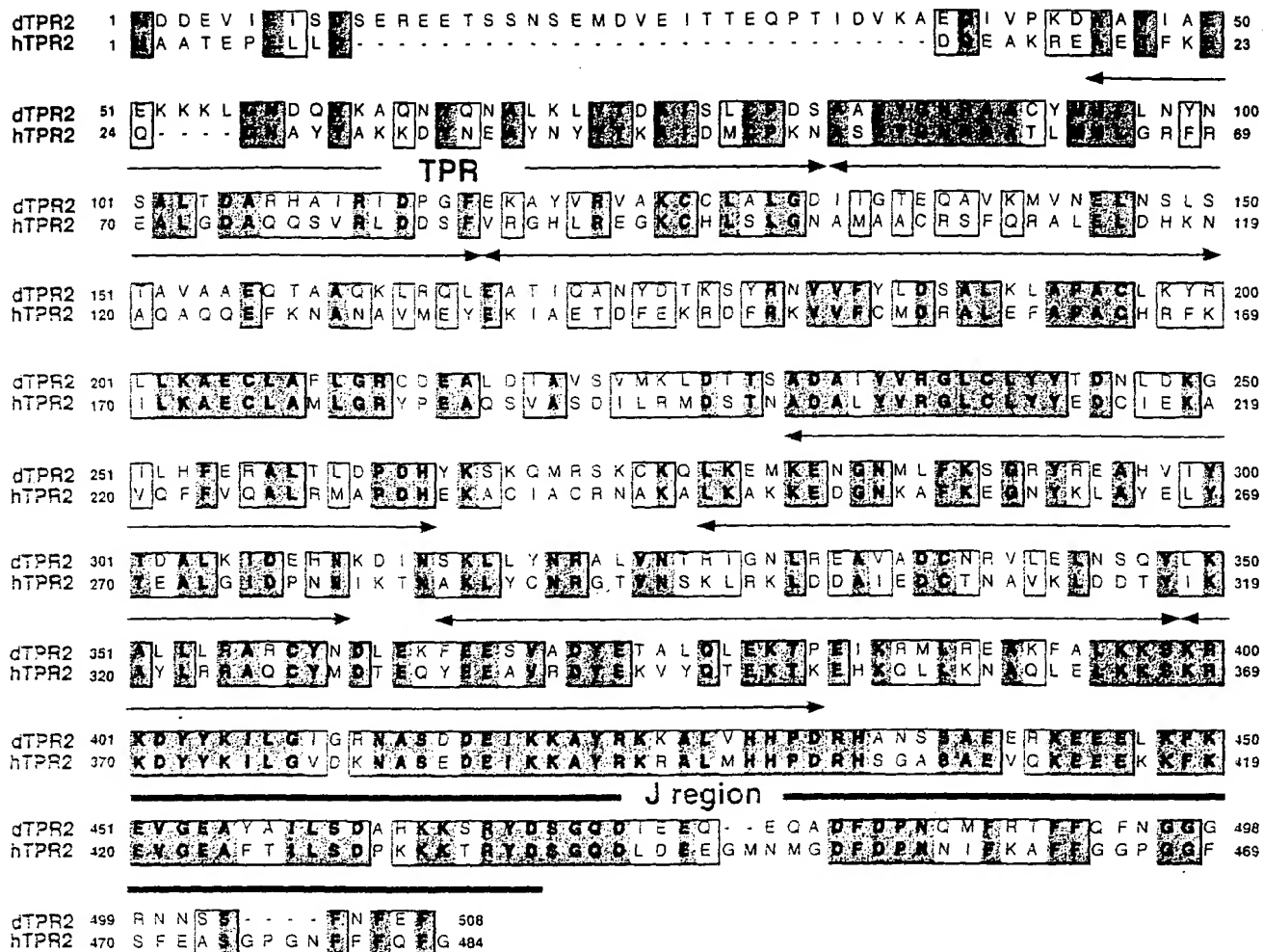
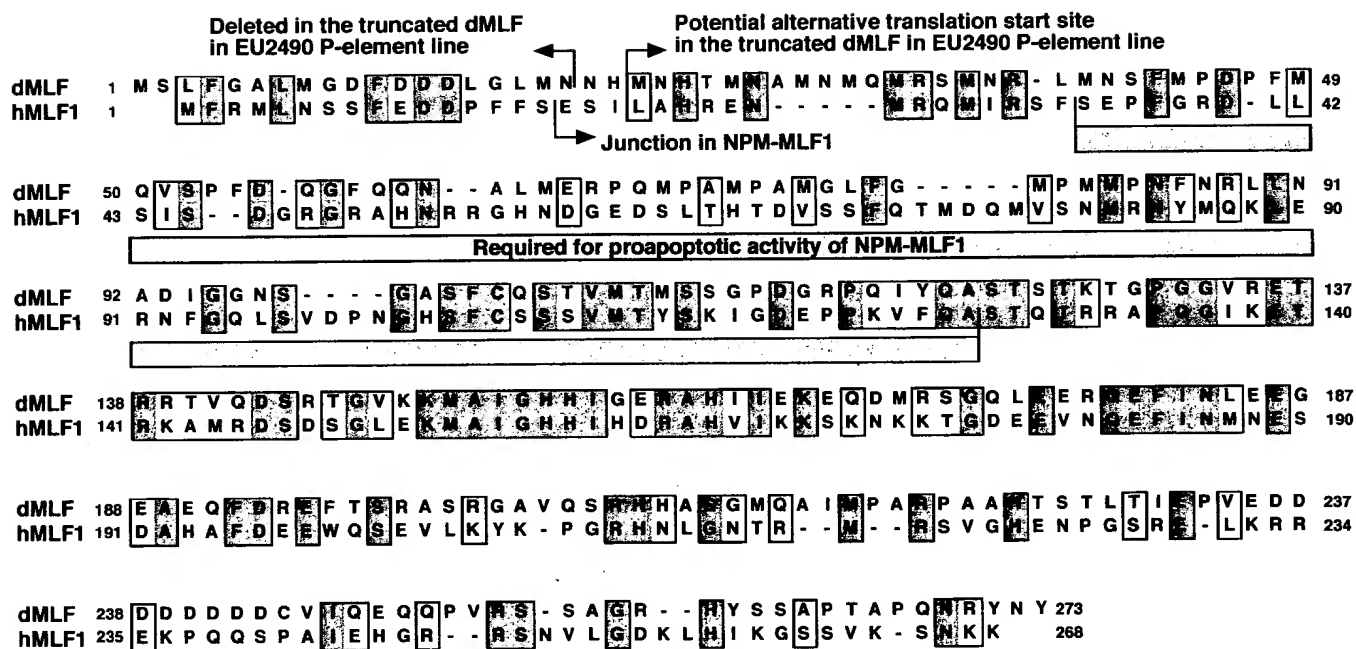


FIGURE 8



000000-000000

FIGURE 9A

dTPR2 Protein 508 amino acids

MDDEVIEISDSEREETSSNSEMDVEITTEQPTIDVKAEQIVPKDAATIAEEKKKLG
NDQYKAQNYQNALKLYTDAISLCPDSAAYYGNRAACYMMLLNYSALTDRH
AIRIDPGFEKAYVRVAKCCALGDIIGTEQAVKVMVNELNSLSTAVAAEQTAAQK
LRQLEATIQANYDTKSYRNVVFYLD SALKLAPACLK YRLLKAECLAFLGRCDEA
LDIAVSVMKLDTTSADAIYVRGLCLYYTDNLDKGILHFERALTDPDPHYKSKQM
RSKCKQLKEMKENG NMLFKSGRYREAHVIYTDALKIDEHNKDINSKLLYNRALV
NTRIGNLREAVADCNRVLELNSQYLKALLLRARCYNDLEKFEESVADYETALQL
EKTPEIKRMLREAKFALKKSKRKDYKILGIGRNASDDEIKKAYRKALVHHPD
RHANSSAEERKEEELKFKEVGEAYAILSDAHKKSR YDSGQDIEEQEQADFPNQ
MFR TFFQFN GGGRNSSFNFEF

FIGURE 9B

dTPR2 cDNA 2239 base pairs

GGCACGAGCCACTACTTCGCATGGCACGCTTTTTTCCGTGTGCTCGGTTCGTT
CGGCCATACAAAACACAAAATTCAAGTTTAAAACTAAATAGGCAACTAAAA
GGGAAGCCGCAGCGAATAAAGTGATTTGCTGAAAGAGACGTAAGAAAAGTTA
ATCGCATCGAAGGCACCAGAAATCGGGGATTTCTAACACGGCGCGCGTGCGA
CGTACATACATACGCAAGCGCACACACACACGAACAATTACTTGCCATTGAC
GCAAAAGCGAAAAAGCAGTGAATAAAGGGGAATTGACAAATAACAACGTT
TTGCAAGCACTGGACTCTGGTCGCTGGTGTTCTTTCATTTTGTAATTGCCACG
CATGGACGACGAAGTAATTGAAATTAGCGACAGCGAACGCGAAGAAACCTC
ATCGAACTCCGAAATGGATGTGGAAATAACGACAGAACAGCCAACCATCGAT
GTCAAAGCAGAGCAAATTGTGCCCAAGGACGCGGCAACCATTGCCGAGGAG
AAGAAGAACTGGGCAACGACCAATACAAGGCGCAGAACTATCAGAATGCA
CTCAAGCTCTACACGGATGCCATATCGCTGTGTCCGGACTCGGCGGCATACTA
TGGCAATCGGGCCGCTGCTACATGATGCTGCTCAACTATAATAGCGCCCTG
ACCGACGCCCCGACACGCCATACGCATCGATCCGGGCTTCGAGAAGGCCTACG
TCCGTGTGGCCAAGTGCTGTCTGGCCCTGGGCGACATTATTGGCACCGAACA
GGCCGTCAAAAATGGTCAACGAGCTGAATTCGCTTAGCACGGCTGTTGCTGCC
GAACAGACGGCGGCGCAAAAGTTGCGCCAATTGGAGGCCACCATTCAGGCG
AACTACGATACGAAATCCTATCGCAATGTGGTCTTCTATTTGGATAGTGCCTT
GAAATTGGCGCCCGCCTGTTTGAAATATCGTCTACTCAAGGCTGAGTGCCTTG
CATTTTTGGGGCGATGTGATGAGGCCTTGACATTGCGGTCAGTGTAATGAA
ACTGGATACCACATCGGCGGATGCGATATACGTGAGAGGTCTGTGCCTGTAC
TACACGGACAACCTGGACAAGGGAATTCTTCATTTTCGAGCGCGCCCTGACCC
TCGACCCGGACCACTACAAGTCCAAGCAGATGCGCAGCAAATGCAAGCAGCT
CAAGGAGATGAAGGAGAACGGCAATATGCTATTCAAGTCGGGTTCGGTATCGC
GAGGCACACGTTATCTACACGGACGCCCTGAAGATCGATGAACACAACAAGG
ATATCAATTCGAAATTGCTTTACAATCGGGCTTTGGTCAACACGCGTATTGGC
AATTTGCGAGAGGCCGTGGCCGATTGCAATCGAGTGCTGGAGCTGAATAGTC
AGTATCTGAAGGCTCTGTTGCTGCGAGCGCGCTGCTACAATGATCTGGAGAA
GTTTCGAGGAGTCGGTGGCGGACTATGAGACGGCGCTGCAGCTGGAGAAGAC
GCCGGAGATTAAGCGAATGCTGCGCGAGGCCAAGTTTGCGTTGAAGAAGTCG
AAGCGAAAGGACTACTACAAGATCCTGGGCATTGGACGCAATGCGTCCGACG
ACGAGATCAAGAAGGCGTATCGCAAAAAGGCGCTGGTACATCATCCGGATCG

[illegible][illegible]

FIGURE 10A

dMLF Protein 273 amino acids

MSLFGALMGDFDDDLGLMNNHNMNHTMNAMNMQMRSMNRLMNSFMPDPFMQ
VSPFDQGFQQNALMERPQMPAMPAMGLFGMPMPNPNRLLNADIGGNSGASF
CQSTVMTMSSGPDGRPQIYQASTSTKTGPGGVRETRRTVQDSRTGVKKMAIGHH
IGERAHIIIEKEQDMRSGQLEERQEFINLEEAEQFDREFTSRASRGAVQSRHHAG
GMQAIMPARPAHTSTLTIEPVEDDDDDDDDCVIEQQPVRSSAGRHYSSAPTAP
QNRNYN

FIGURE 10B

dMLF cDNA 1753 base pairs

GGCACGAGGAAAATATTCGTGAAAATTCTGCATACGGAAAGAAGAAAATTC
GAGCAACAGAAAGCCAACACAATCCACAAAAATGTCTTTATTCGGAGCGTTG
ATGGGTGATTTTCGACGACGATCTCGGCCTTATGAACAACCACATGAACCACA
CTATGAACGCGATGAACATGCAGATGCGCTCGATGAATCGCCTGATGAACAG
CTTTATGCCCCGATCCCTTCATGCAGGTCTCGCCCTTTGACCAGGGATTCCAGC
AGAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCATGCCAGCCATGGGCCT
CTTCGGCATGCCCATGATGCCAACTTTAATCGCCTGTTGAACGCTGATATTG
GTGGCAATTCAGGCGCATCCTTCTGCCAGAGCACCGTGATGACCATGTCATC
GGGTCCCGATGGGCGTCCTCAGATCTACCAGGCCAGCACTAGTACCAAAACA
GGACCGGGAGGCGTTCTGTGAGACCCGCAGGACGGTGCAGGACTCGCGCACT
GGGGTGAAGAAGATGGCCATTGGTCATCACATCGGCGAGCGGGCACACATTA
TTGAGAAAGAGCAGGACATGCGCTCAGGACAACCTGGAGGAGCGCCAGGAGT
TCATTAATCTGGAGGAGGGAGAAGCCGAGCAGTTTGACAGGGAGTTTACATC
GCGCGCTAGTCGCGGAGCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAG
GCCATCATGCCCCGCCGTCCAGCGGCACACACCTCGACGTTGACCATTGAGC
CAGTGGAGGACGACGACGACGATGATGATGACTGTGTAATCCAGGAGCAGC
AACCGGTTCTGCTCCTCCGCGGGCCGCCATTATTCCAGTGCGCCAACGGCACC
GCAGAACAGATATAATTACTAAATCTAAAGTCAATACAGTATATTTTACTAA
CTATCCGATAAAACAGAAACAGAATTGCATACTATAAATTTCTGCTAATTAC
ATTCCCAACTGCGTTCAAACGAAACGAATATCGAATCGAAATCATAGAATGC
ACAGAGCAGCATACATCCACATCCCTATGCCGCCAATCCGAGGCGCCAACAA
CGTGCCGTAAAACATTTTACACGAGGACGAAGCGGCCAGCTCCTACAAGG
CGGTCAAGCGCGGCAAGAAGAAGTAGTAGAAACGTGATCATCTGTATGCCAA
CATCTTCCGCATCGCACACTCAAAAACACTAGGAAGCAAAGCGTTGGGTTCT
GTTCCATAGCAGGAAAACCAATTCAAATATTTTTTAACAAACACAATTCTTTA
CCAGTTCTGTCTTATCCTGCGTGAGTCGACCAGAATGCAACACTAAAAAATGT
ACAACTTCAAGATGCTATTGATGTGCACGCAGGATACAGAACAACCTTGCTTA
AATTTACTTAAAACAAATGTGACTATTCAACGCCGAAATCATTACAACACAC
ACTCTCAGACCTAATCGAAAAATTCAATGAAAGTAATGGAATATATATGAAA
TCGTAATTATAAGTTTGAATTATTTGATTAATTCTCAAGTTTTTAGATTTTGT
AGCCACTAAGCTTTAAATTATGGATGCCAGTTAGCGTGCAAATGAACACAAT
TGATTTGAAGGCTCCGAACGATAGAAAACAACAATTACCAATTCCCCAAATA
CATGTAATTCGTAAGGCCTAAGTAAATGTTAACGTGAATTTAATTAAATGGTA
ATTACATTATAATAGTAAAAAAAAAAAAAAAAAAAA

ClustalW Formatted Alignments

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AA950779 | 123 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI458556 | 127 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI457049 | 127 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI110008 | 130 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA201154 | 132 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA952015 | 132 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI516974 | 138 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA201429 | 132 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA392620 | 129 | A | C | T | T | G | C | A | T | T | T | T | G | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | T | | |
| AA439655 | 111 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI544064 | 114 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AI516760 | 113 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA978757 | 113 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA202799 | 113 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA735405 | 115 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA201527 | 118 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | T | C | G | C | A | T | C | G | A | A | G | G | C | A | C | A | G | A | A | T | C | G | G | G | A | T | T | C | T |
| AA438619 | 117 | A | G | A | C | G | T | A | A | G | A | A | G | T | T | A | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Figure 1 consists of 12 histograms arranged in a single row. Each histogram represents the distribution of the number of non-zero elements in the vector x for a specific value of n , ranging from 10 to 120 in increments of 10. The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count' and ranges from 0 to 100. As n increases, the distribution of x becomes more concentrated around zero, with the peak count increasing significantly.

[illegible][illegible][illegible][illegible]

[illegible]

AA950779
A1458556
A1457049
A1110008
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dTPR2 (GH09432) GenBank submit

420 G A A A A A C G A C A G A A C A G C C A A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
274
424 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
428 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
432 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
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387
412 A T A T C C T G C C G C T G T C T A G C G C G A C T T C T G T G A G C A T C C G A C A G T A T
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418 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
368
409 G A A A T A A C G A C A G A A C A G C C A A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
371
378
419 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
413 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
417 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T
421 A T A T C C T G C C G C T G T C T A C C G C G A C T T C T G T G A G C A T C C G A C A G T A T
425 G A A A T A A C C A A C A G A A A C C A C C A C C A C C A T C G A T G T C A A A G C A G A G C A A A T T G T

AA0950779
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AI457049
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AI516760
AA978757
AA202799
AA735495
AA201527
AA438619
AI516274
AA440018
AA820977
AI555605
dTPR2 (GH9432) GenBank submit

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AA202799
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AA820977
AI455565
dTPR2 (GH09432) GenBank submit

FIGURE 11A (Continued)

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 570 | G C C A T A T C G C T | 540 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 545 |
| AI110008 | 577 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G | 525 |
| AA201154 | 530 | | 520 |
| AA952015 | 577 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 525 |
| AI516974 | 586 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 534 |
| AA201429 | 387 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 556 | G C C A T A T C G C T G T G | 549 |
| AI544064 | 580 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 529 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 589 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 519 |
| AA440018 | 583 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 513 |
| AA820977 | 589 | G C C A T A T C G C T G T G T C C G G A | 588 |
| AI455565 | 586 | | 585 |
| dTPR2 (GH09432) GenBank submit | 589 | G C C A T A T C G C T G T G T C C G G A C T C G G C G G C A T A C T A T G G C A A T C G G G C C G C | 537 |

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 540 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 545 |
| AI110008 | 626 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C G C C C G A C | 675 |
| AA201154 | 530 | | 520 |
| AA952015 | 627 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C G C C C G A C | 676 |
| AI516974 | 626 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C | 677 |
| AA201429 | 387 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 549 |
| AI544064 | 610 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C G C C C G A C | 651 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 619 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C G C C C G A C | 649 |
| AA440018 | 613 | C T G C T A C A T G A T G C T G C T C A A C T | 643 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 585 |
| dTPR2 (GH09432) GenBank submit | 626 | C T G C T A C A T G A T G C T G C T C A A C T A T A A T A G C G C C C T G A C C G A C G C C C G A C | 647 |

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 540 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 545 |
| AI110008 | 676 | A C G | 675 |
| AA201154 | 530 | | 520 |
| AA952015 | 677 | A C G C C A T A C G C A T C G A T C C G G G C T T C G A G A A G G C C T A C G T C C G T G T G G C C | 726 |
| AI516974 | 678 | | 677 |
| AA201429 | 387 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 549 |
| AI544064 | 680 | A C G C C A T A C G C A T C G A T C C G G G C T T C G A G | 689 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 689 | A C G C C A T A C G C A T C G A T C C G G G C | 691 |
| AA440018 | 635 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 585 |
| dTPR2 (GH09432) GenBank submit | 688 | A C G C C A T A C G C A T C G A T C C G G G C T T C G A G A A G G C C T A C G T C C G T G T G G C C | 737 |

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 540 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 545 |
| AI110008 | 679 | | 678 |
| AA201154 | 530 | | 520 |
| AA952015 | 727 | A A G T G C T G T C T G G C C C T G G G C G A C A T T A T T G G C C C G A A C A G G C C G T C A A A | 776 |
| AI516974 | 678 | | 677 |
| AA201429 | 387 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 549 |
| AI544064 | 689 | | 688 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 692 | | 691 |
| AA440018 | 635 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 585 |
| dTPR2 (GH09432) GenBank submit | 728 | A A G T G C T G T C T G G C C C T G G G C G A C A T T A T T G G C A C C G A A C A G G C C G T C A A | 787 |

FIGURE 11A (Continued)

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 580 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 565 |
| AI110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 777 | A T G G T T | 782 |
| AI516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| AI544064 | 689 | | 688 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 788 | A A T G G T C A A C G A G C T G A A T T C G C T T A G C A C G G C T G T T G C T G C C G A A C A G A | 837 |

| | | | |
|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 580 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 565 |
| AI110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| AI516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| AI544064 | 689 | | 688 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 838 | C G G C G G C G C A A A A G T T G C G C C A A T T G G A G G C C A C C A T T C A G G C G A A C T A C | 887 |

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|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 580 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 565 |
| AI110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| AI516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| AI544064 | 689 | | 688 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 888 | G A T A C G A A A T C C T A T C G C A A T G T G G T C T T C T A T T T G G A T A G T G C C T T G A A | 937 |

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|--------------------------------|-----|---|-----|
| AA950779 | 581 | | 580 |
| AI456556 | 274 | | 273 |
| AI457049 | 586 | | 565 |
| AI110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| AI516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| AI544064 | 689 | | 688 |
| AI516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| AI516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| AI455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 938 | A T T G G C G C C C G C C T G T T T G A A A T A T C G T C T A C T C A A G G C T G A G T G C C T T G | 987 |

GenBank accession numbers

FIGURE 11A (Continued)

| | | |
|--------------------------------|-----|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 588 | 1037 |

C A T T T T T G G G G C G A T G T G A T G A G G C C T T G G A C A T T G C G G T C A G T G T A A T G

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1038 | 1087 |

A A A C T G G A T A C C A C A T C G G C G G A T G C G A T A T A C G T G A G A G G T C T G T G C C T

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1088 | 1137 |

G T A C T A C A C G G A C A A C C T G G A C A A G G G A A T T C T T C A T T T C G A G C G C G C C C

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1138 | 1187 |

T G A C C C T C G A C C C G G A C C A C T A C A A G T C C A A G C A G A T G C G C A G C A A A T G C

FIGURE 11A (Continued)

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 586 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1188 | 1237 |

A A G C A G C T C A A G G A G A T G A A G G A G A A C G G C A A T A T G C T A T T C A A G T C G G G

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 586 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1238 | 1287 |

T C G G T A T C G C G A G G C A C A C G T T A T C T A C A C G G A C G C C C T G A A G A T C G A T G

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 586 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1288 | 1337 |

A A C A C A A C A A G G A T A T C A A T T C G A A A T T G C T T T A C A A T C G G G C T T T G G T C

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|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 586 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1338 | 1387 |

A A C A C G C G T A T T G G C A A T T T G C G A G A G G C C G T G G C C G A T T G C A A T C G A G T

FIGURE 11A (Continued)

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
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| A1457049 | 586 | 565 |
| A1110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| A1516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| A1544064 | 689 | 688 |
| A1516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| A1516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| A1455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1388 | 1437 |

G C T G G A G C T G A A T A G T C A G T A T C T G A A G G C T C T G T T G C T G C G A G C G C G C T

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| A1456556 | 274 | 273 |
| A1457049 | 586 | 565 |
| A1110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| A1516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| A1544064 | 689 | 688 |
| A1516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| A1516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| A1455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1438 | 1487 |

G C T A C A A T G A T C T G G A G A A G T T C G A G G A G T C G G T G G C G G A C T A T G A G A C G

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| A1456556 | 274 | 273 |
| A1457049 | 586 | 565 |
| A1110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| A1516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| A1544064 | 689 | 688 |
| A1516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| A1516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| A1455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1488 | 1537 |

G C G C T G C A G C T G G A G A A G A C G C C G G A G A T T A A G C G A A T G C T G C G C G A G G C

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| A1456556 | 274 | 273 |
| A1457049 | 586 | 565 |
| A1110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| A1516974 | 678 | 677 |
| AA201429 | 367 | 386 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| A1544064 | 689 | 688 |
| A1516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| A1516274 | 682 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| A1455565 | 586 | 565 |
| dTPR2 (GH09432) GenBank submit | 1538 | 1587 |

C A A G T T T G C G T T G A A G A A G T C G A A G C G A A A G G A C T A C T A C A A G A T C C T G G

FIGURE 11A (Continued)

| | | | |
|--------------------------------|------|---|------|
| AA950779 | 581 | | 580 |
| A1456556 | 274 | | 273 |
| A1457049 | 586 | | 565 |
| A1110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| A1516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| A1544064 | 689 | | 688 |
| A1516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| A1516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| A1455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 1588 | G C A T T G G A C G C A A T G C G T C C G A C G A C G A G A T C A A G A A G G C G T A T C G C A A A | 1637 |

| | | | |
|--------------------------------|------|---|------|
| AA950779 | 581 | | 580 |
| A1456556 | 274 | | 273 |
| A1457049 | 586 | | 565 |
| A1110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| A1516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| A1544064 | 689 | | 688 |
| A1516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| A1516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| A1455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 1638 | A A G G C G C T G G T A C A T C A T C C G G A T C G A C A C G C A A A C A G C A G T G C C G A G G A | 1687 |

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|--------------------------------|------|---|------|
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| A1456556 | 274 | | 273 |
| A1457049 | 586 | | 565 |
| A1110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| A1516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| A1544064 | 689 | | 688 |
| A1516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| A1516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| A1455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 1688 | G C G C A A G G A G G A G G A G C T C A A G T T C A A G G A G G T G G G C G A G G C G T A C G C C A | 1737 |

| | | | |
|--------------------------------|------|---|------|
| AA950779 | 581 | | 580 |
| A1456556 | 274 | | 273 |
| A1457049 | 586 | | 565 |
| A1110008 | 679 | | 678 |
| AA201154 | 530 | | 529 |
| AA952015 | 783 | | 782 |
| A1516974 | 678 | | 677 |
| AA201429 | 367 | | 386 |
| AA392620 | 535 | | 534 |
| AA439655 | 570 | | 569 |
| A1544064 | 689 | | 688 |
| A1516760 | 532 | | 531 |
| AA978757 | 480 | | 479 |
| AA202799 | 368 | | 367 |
| AA735495 | 504 | | 503 |
| AA201527 | 371 | | 370 |
| AA438619 | 378 | | 377 |
| A1516274 | 692 | | 691 |
| AA440018 | 636 | | 635 |
| AA820977 | 589 | | 588 |
| A1455565 | 586 | | 565 |
| dTPR2 (GH09432) GenBank submit | 1738 | T A C T G T C G G A T G C T C A C A A G A A G T C G C G C T A C G A C A G C G G C C A G G A T A T C | 1787 |

FIGURE 11A (Continued)

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 681 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1788 | 1837 |

G A G G A G C A G G A G C A A G C C G A C T T C G A T C C G A A T C A A A T G T T C C G C A C A T T

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 681 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1838 | 1887 |

C T T C C A A T T C A A C G G C G G T G G C C G G A A T A A T T C A T C G T T C A A C T T T G A G T

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 681 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1888 | 1937 |

T C T A G G A T C C C A A C G A G T G T T G T T C A C C A C C A C A G A G A A G A A G A C C A T C T

| | | |
|--------------------------------|------|------|
| AA950779 | 581 | 580 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 682 | 681 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submit | 1938 | 1987 |

C A A T C C C A T A C T T T C T G C C T C A T C C G A A A C C A A C A T A C A G C A G C G C A C A A

FIGURE 11A (Continued)

| | | |
|---------------------------------|------|------|
| AA950779 | 561 | 560 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submitt | 1988 | 2037 |

ATTTTGAAC TCTTTTACATATTTCTTTTCCAAAAAGCAAGAAAAATACCAC

| | | |
|---------------------------------|------|------|
| AA950779 | 561 | 560 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submitt | 2238 | 2087 |

ATTTTGATTATGTTAACGAATGAATATATGCCAAGTTATTTGAAAAAATA

| | | |
|---------------------------------|------|------|
| AA950779 | 561 | 560 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submitt | 2088 | 2137 |

TTCTAAATCAAAATAATGCAACTAAATTTCCAGTGTAAGTTCACATTTTT

| | | |
|---------------------------------|------|------|
| AA950779 | 561 | 560 |
| AI456556 | 274 | 273 |
| AI457049 | 566 | 565 |
| AI110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| AI516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| AI544064 | 689 | 688 |
| AI516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| AI516274 | 692 | 691 |
| AA440018 | 636 | 635 |
| AA820977 | 589 | 588 |
| AI455565 | 566 | 565 |
| dTPR2 (GH09432) GenBank submitt | 2138 | 2187 |

AAATGTTCTTTCTTGGAATTTTTTTTTTCGGCAACATTAATAAATCATGGGA

[illegible][illegible]

| | | |
|--------------------------------|------|----------|
| AA950779 | 591 | 590 |
| A1456556 | 274 | 273 |
| A1457049 | 596 | 595 |
| A1110008 | 679 | 678 |
| AA201154 | 530 | 529 |
| AA952015 | 783 | 782 |
| A1516974 | 678 | 677 |
| AA201429 | 367 | 366 |
| AA392620 | 535 | 534 |
| AA439655 | 570 | 569 |
| A1544064 | 689 | 688 |
| A1516760 | 532 | 531 |
| AA978757 | 480 | 479 |
| AA202799 | 368 | 367 |
| AA735495 | 504 | 503 |
| AA201527 | 371 | 370 |
| AA438619 | 378 | 377 |
| A1516274 | 682 | 681 |
| AA440018 | 636 | 635 |
| AA820977 | 595 | 594 |
| A1555565 | 599 | 598 |
| dTPP2 (GH09432) GenBank submit | 2238 | A A 2239 |

ClustalW Formatted Alignments

A1456052 40 T C G C T G T T C G G A C T C G G C G G C A T A C T A T G G C A A T T C G G G C C G C C T T G C T A
 AA391402 70 T C G C T G T T C G G A C T C G G C G G C A T A C T A T G G C A A T T C G G G C C G C C T T G C T A
 A1514849 151 T C G C T G T T C G G A C T C G G C G G C A T A C T A T G G C A A T T C G G G C C G C C T T G C T A
 A1519786 150 T C G C T G T T C G G A C T C G G C G G C A T A C T A T G G C A A T T C G G G C C G C C T T G C T A
 A1546378 48 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA438290 57 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA820520 57 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA941597 57 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 A1455870 57 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA950277 57 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA941028 61 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA951077 66 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA951083 73 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA949900 73 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA541065 74 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 AA441093 74 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A
 dTPR2 (GH09432) GenBank submit 104 A A G G G A A G C C G C A G C G A - A T A A A G T G A T T T G C T G A A A G A G A C G T A A G A A A

FIGURE 11B (Continued)

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------------------------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|
| AI456052 | 90 | C | A | T | G | A | T | G | C | T | G | C | T | C | A | A | C | T | A | T | A | A | T | A | G | C | G | C | C | T | G | A | C | C | G | A | C | G | C | C | G | A | C | A | C | G | C | C | A | 120 |
| AA391402 | 120 | C | A | T | G | A | T | G | C | T | G | C | T | C | A | A | C | T | A | T | A | A | T | A | G | C | G | C | C | T | G | A | C | C | G | A | C | G | C | C | G | A | C | A | C | G | C | C | A | 150 |
| AI514849 | 201 | C | A | T | G | A | T | G | C | T | G | C | T | C | A | A | C | T | A | T | A | A | T | A | G | C | G | C | C | T | G | A | C | C | G | A | C | G | C | C | G | A | C | A | C | G | C | C | A | 250 |
| AI519786 | 200 | C | A | T | G | A | T | G | C | T | G | C | T | C | A | A | C | T | A | T | A | A | T | A | G | C | G | C | C | T | G | A | C | C | G | A | C | G | C | C | G | A | C | A | C | G | C | C | A | 240 |
| AI546378 | 97 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 142 |
| AA438290 | 106 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 152 |
| AA820520 | 106 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 152 |
| AA941597 | 106 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 152 |
| AI455870 | 106 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 152 |
| AA950277 | 106 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 152 |
| AA941028 | 110 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 155 |
| AA951077 | 115 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 161 |
| AA951083 | 122 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 166 |
| AA949900 | 122 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 166 |
| AA541065 | 123 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 166 |
| AA441093 | 123 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 166 |
| dTPR2 (GH09432) GenBank submitt | 153 | G | T | T | A | A | T | C | G | C | A | - | T | C | G | A | A | G | G | C | A | C | C | A | G | A | A | T | C | G | G | - | G | A | T | T | T | C | T | A | A | C | A | C | G | G | C | G | - | 169 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------------------------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|
| AI456052 | 140 | T | A | C | G | C | A | T | C | G | A | T | C | C | G | G | G | C | T | T | C | G | A | G | A | G | G | C | T | A | C | G | T | C | C | G | T | G | T | G | G | C | A | A | G | T | G | C | 186 |
| AA391402 | 170 | T | A | C | G | C | A | T | C | G | A | T | C | C | G | G | G | C | T | T | C | G | A | G | A | G | G | C | T | A | C | G | T | C | C | G | T | G | T | G | G | C | A | A | G | T | G | C | 216 |
| AI514849 | 251 | T | A | C | G | C | A | T | C | G | A | T | C | C | G | G | G | C | T | T | C | G | A | G | A | G | G | C | T | A | C | G | T | C | C | G | T | G | T | G | G | C | A | A | G | T | G | C | 300 |
| AI519786 | 250 | T | A | C | G | C | A | T | C | G | A | T | C | C | G | G | G | C | T | T | C | G | A | G | A | G | G | C | T | A | C | G | T | C | C | G | T | G | T | G | G | C | A | A | G | T | G | C | 284 |
| AI546378 | 144 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 163 |
| AA438290 | 153 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 202 |
| AA820520 | 153 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 202 |
| AA941597 | 153 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 202 |
| AI455870 | 153 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 202 |
| AA950277 | 153 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 202 |
| AA941028 | 157 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 206 |
| AA951077 | 162 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 211 |
| AA951083 | 169 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 170 |
| AA949900 | 169 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 214 |
| AA541065 | 170 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 214 |
| AA441093 | 170 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 240 |
| dTPR2 (GH09432) GenBank submitt | 200 | C | C | G | T | G | C | G | A | C | G | T | A | C | A | T | A | C | A | T | A | C | G | C | A | A | G | C | G | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | A | C | 240 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|
| AI456052 | 190 | T | G | T | C | T | G | G | C | C | T | G | G | G | C | G | A | C | A | T | T | T | G | G | C | A | C | C | G | A | A | C | A | G | G | C | C | G | T | C | A | A | A | A | T | G | G | T | 234 |
| AA391402 | 220 | T | G | T | C | T | G | G | C | C | T | G | G | G | C | G | A | C | A | T | T | T | G | G | C | A | C | C | G | A | A | C | A | G | G | C | C | G | T | C | A | A | A | A | T | G | G | T | 266 |
| AI514849 | 301 | T | G | T | C | T | G | G | C | C | T | G | G | G | C | G | A | C | A | T | T | T | G | G | C | A | C | C | G | A | A | C | A | G | G | C | C | G | T | C | A | A | A | A | T | G | G | T | 350 |
| AI519786 | 300 | T | G | T | C | T | G | G | C | C | T | G | G | G | C | G | A | C | A | T | T | T | G | G | C | A | C | C | G | A | A | C | A | G | G | C | C | G | T | C | A | A | A | A | T | G | G | T | 348 |
| AI546378 | 194 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 242 | |
| AA438290 | 203 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 251 | |
| AA820520 | 203 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 251 |
| AA941597 | 203 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 251 |
| AI455870 | 203 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 251 |
| AA950277 | 203 | T | T | G | C | C | A | T | T | G | A | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | 255 |
| AA941028 | 207 | T | T | G | C | C | A | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

[illegible]

430 T T G G G G G A T T G T G A T G G G C C T T G G A C A T T G C G G T C A G T G T A A T G A A A C T 488
488 T T T G G G G G C A T T G T G A T G A G G C C T T G G A C A T T G C G G T C A G T G T A A T G A A A C T 517
550 T T T G G G G G C A T T G T G A T G A G G C C T T G G A C A T T G C G G T C A G T G T A A T G A A A C T 559
548 T T G G G G C A T T G T G A T G A G G C C T T G G A C A T T G C G G T C A G T G T A A T G A A A C T 561
436 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 494
443 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 491
444 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 492
445 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 493
445 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 493
445 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 493
448 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G 497
247 245
171 170
460 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 505
458 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 506
459 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 507
462 A A G G A C G C G G C A A C C A T T G C C G A G G A G A A G A A A C T G G G C A A C G A C C 540

FIGURE 11B (Continued)

| | | | | | | | | | | | | | | |
|--------------------------------|-----|---|-----|--------|------|------|-------|-----|-----|-----|------|-----|-----|-----|
| AI456052 | 489 | GGATACCACAT | CGG | CGGATG | CGAT | ATAC | GTGAG | AGG | TCT | GTG | CTGT | ACT | 536 | |
| AA391402 | 518 | GGATACCACAT | CGG | CGGATG | CGAT | ATAC | GTGAG | AGG | TCT | GTG | CTGT | ACT | 567 | |
| AI514849 | 600 | GGATACCACAT | CGG | CGGATG | CGAT | ATAC | GTGA | | | | | | 621 | |
| AI519786 | 562 | | | | | | | | | | | | 561 | |
| AI546378 | 485 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 554 |
| AA438290 | 492 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 541 |
| AA820520 | 493 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 542 |
| AA941597 | 494 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 543 |
| AI455870 | 494 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 545 |
| AA950277 | 494 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 542 |
| AA941028 | 488 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 487 |
| AA951077 | 247 | | | | | | | | | | | | | 246 |
| AA951083 | 171 | | | | | | | | | | | | | 170 |
| AA949900 | 509 | AAT | | | | | | | | | | | | 511 |
| AA541065 | 507 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 555 |
| AA441093 | 508 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 557 |
| dTPR2 (GH09432) GenBank submit | 541 | AATACAAAGGCGCAGAACTATCAGAATGCACTCAAGCTCTACACGGATGCC | | | | | | | | | | | | 550 |

| | | | | |
|--------------------------------|-----|--------|---|-----|
| AI456052 | 539 | ACACGG | ACAACTGGACAAGGGAATTCTTTCATTTTCGAGCGCGCCCTGACC | 586 |
| AA391402 | 558 | ACACGG | ACAACTGGACAAGGGAATTCTTTCATTTTCGAGCGCGCCCTGACC | 617 |
| AI514849 | 632 | | | 631 |
| AI519786 | 562 | | | 561 |
| AI546378 | 535 | ATA | TCC | 541 |
| AA438290 | 542 | ATA | TCC | 540 |
| AA820520 | 543 | ATA | TCC | 502 |
| AA941597 | 544 | ATA | TCC | 502 |
| AI455870 | 544 | ATA | TCC | 502 |
| AA950277 | 544 | ATA | TCC | 502 |
| AA941028 | 488 | ATA | TCC | 487 |
| AA951077 | 247 | | | 246 |
| AA951083 | 171 | | | 170 |
| AA949900 | 512 | | | 511 |
| AA541065 | 557 | ATA | TCC | 555 |
| AA441093 | 558 | ATA | TCC | 557 |
| dTPR2 (GH09432) GenBank submit | 591 | ATA | TCC | 557 |

| | | | |
|--------------------------------|-----|--|-----|
| AI456052 | 599 | C | 585 |
| AA391402 | 618 | CTCGACCCGGGACCCTACCAGTCCAAGCAGATGCGC | 657 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 593 | CTACATGATGCTGCTCAACTATAAT | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 607 | CTACATGATGCTGCTCAACTATAATAGCGCCCTGACCGACGCCCGACACG | 655 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 641 | CTACATGATGCTGCTCAACTATAATAGCGCCCTGACCGACGCCCGACACG | 691 |

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|--------------------------------|-----|---|-----|
| AI456052 | 590 | | 585 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 657 | CCATACGCATCGATCCGGGCTTCGAGAAGGCCTACGTCCGTGT | 655 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 691 | CCATACGCATCGATCCGGGCTTCGAGAAGGCCTACGTCCGTGTGGCCAAAG | 743 |

GenBank accession numbers

FIGURE 11B (Continued)

| | | |
|--------------------------------|-----|-----|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 741 | 740 |

T G C T G T C T G G C C C T G G G C G A C A T T A T T G G C A C C G A A C A G G C C G T C A A A A T

| | | |
|--------------------------------|-----|-----|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 791 | 790 |

G G T C A A C G A G C T G A A T T C G C T T A G C A C G G C T G T T G C T G C C G A A C A G A C G G

| | | |
|--------------------------------|-----|-----|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 841 | 840 |

C G G C G C A A A A G T T G C G C C A A T T G G A G G C C A C C A T T C A G G C G A A C T A C G A T

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|--------------------------------|-----|-----|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 891 | 890 |

A C G A A A T C C T A T C G C A A T G T G G T C T T C T A T T T G G A T A G T G C C T T G A A A T T

FIGURE 11B (Continued)

| | | |
|---|-----|-----|
| AI456052 | 590 | 585 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 941 | 939 |
| G G C G C C C G C C T G T T T G A A A T A T C G T C T A C T C A A G G C T G A G T G C C T T G C A T | | |

| | | |
|---|-----|------|
| AI456052 | 590 | 585 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 991 | 1029 |
| T T T T G G G G C G A T G T G A T G A G G C C T T G G A C A T T G C G G T C A G T G T A A T G A A A | | |

| | | |
|---|------|------|
| AI456052 | 590 | 585 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1041 | 1074 |
| C T G G A T A C C A C A T C G G C G G A T G C G A T A T A C G T G A G A G G T C T G T G C C T G T A | | |

| | | |
|---|------|------|
| AI456052 | 590 | 585 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1091 | 1140 |
| C T A C A C G G A C A A C C T G G A C A A G G G A A T T C T T C A T T T C G A G C G C G C C C T G A | | |

FIGURE 11B (Continued)

| | | | |
|--------------------------------|------|--|------|
| AI456052 | 590 | | 590 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1141 | CCCTCGACCCGGACCACTACAAGTCCAAGCAGATGCGCAGCAAATGCAAG | 1140 |

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1191 | CAGCTCAAGGAGATGAAGGAGAACGGCAATATGCTATTCAAGTCGGGTCTG | 1190 |

| | | | |
|--------------------------------|------|--|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1241 | GTATCGCGAGGCACACGTTATCTACACGGACGCCCTGAAGATCGATGAAC | 1240 |

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1291 | ACAACAAGGATATCAATTTCGAAATTGCTTTACAATCGGGCTTTGGTCAAC | 1290 |

GenBank accession numbers

FIGURE 11B (Continued)

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1341 | 1340 |

ACGCGTATTGGCAATTTGCGAGAGGCCGTGGCCGATTGCAATCGAGTGTCT

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1391 | 1390 |

GGAGCTGAATAGTCAGTATCTGAAGGCTCTGTTGCTGCGAGCGCGCTGTCT

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1441 | 1440 |

ACAAATGATCTGGAGAAGTTTCGAGGAGTCGGTGGCGGACTATGAGACGGCG

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1491 | 1490 |

CTGCAGCTGGAGAAGACGCCGGAGATTAAGCGAATGCTGCGCGAGGCCAA

FIGURE 11B (Continued)

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1541 | 1540 |

G T T T G C G T T G A A G A A G T C G A A G C G A A A G G A C T A C T A C A A G A T C C T G G G C A

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1591 | 1590 |

T T G G A C G C A A T G C G T C C G A C G A C G A G A T C A A G A A G G C G T A T C G C A A A A A G

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1641 | 1640 |

G C G C T G G T A C A T C A T C C G G A T C G A C A C G C A A A C A G C A G T G C C G A G G A G C G

| | | |
|--------------------------------|------|------|
| AI456052 | 590 | 589 |
| AA391402 | 654 | 653 |
| AI514849 | 632 | 631 |
| AI519786 | 562 | 561 |
| AI546378 | 542 | 541 |
| AA438290 | 561 | 560 |
| AA820520 | 618 | 617 |
| AA941597 | 583 | 582 |
| AI455870 | 551 | 550 |
| AA950277 | 547 | 546 |
| AA941028 | 488 | 487 |
| AA951077 | 247 | 246 |
| AA951083 | 171 | 170 |
| AA949900 | 512 | 511 |
| AA541065 | 700 | 699 |
| AA441093 | 597 | 596 |
| dTPR2 (GH09432) GenBank submit | 1691 | 1690 |

C A A G G A G G A G G A G C T C A A G T T C A A G G A G G T G G G C G A G G C G T A C G C C A T A C

FIGURE 11B (Continued)

| | | | |
|---------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submitt | 1741 | T G T C G G A T G C T C A C A A G A A G T C G C G C T A C G A C A G C G G C C A G G A T A T C G A G | 1740 |

| | | | |
|---------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submitt | 1791 | G A G C A G G A G C A A G C C G A C T T C G A T C C G A A T C A A A T G T T C C G C A C A T T C T T | 1790 |

| | | | |
|---------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submitt | 1841 | C C A A T T C A A C G G C G G T G G C C G G A A T A A T T C A T C G T T C A A C T T T G A G T T C T | 1840 |

| | | | |
|---------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submitt | 1891 | A G G A T C C C A A C G A G T G T T G T T C A C C A C C A C A G A G A A G A A G A C C A T C T C A A | 1890 |

GenBank accession numbers

FIGURE 11B (Continued)

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1941 | T C C C A T A C T T T T C T G C C T C A T C C G A A A C C A A C A T A C A G C A G C G C A C A A A T T | 1991 |

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 1991 | T T G A A C T C T T T T T A C A T A T T T C T T T T T C C A A A A A G C A A G A A A A T A C C A C A T T | 2041 |

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 2041 | T T G A T T A T G T T A A C G A A T G A A T A T A T G C C A A G T T A T T T G A A A A A A T A T T C | 2091 |

| | | | |
|--------------------------------|------|---|------|
| AI456052 | 590 | | 589 |
| AA391402 | 654 | | 653 |
| AI514849 | 632 | | 631 |
| AI519786 | 562 | | 561 |
| AI546378 | 542 | | 541 |
| AA438290 | 561 | | 560 |
| AA820520 | 618 | | 617 |
| AA941597 | 583 | | 582 |
| AI455870 | 551 | | 550 |
| AA950277 | 547 | | 546 |
| AA941028 | 488 | | 487 |
| AA951077 | 247 | | 246 |
| AA951083 | 171 | | 170 |
| AA949900 | 512 | | 511 |
| AA541065 | 700 | | 699 |
| AA441093 | 597 | | 596 |
| dTPR2 (GH09432) GenBank submit | 2091 | T A A A T C A A A A T A A T G C A A C T A A A T T T C C A G T G T A A G T T C A C A T T T T T A A A | 2141 |

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FIGURE 11B (Continued)

| Accession | Length | Sequence |
|--------------------------------|--------|---|
| AI456052 | 590 | |
| AA391402 | 654 | |
| AI514849 | 632 | |
| AI519786 | 562 | |
| AI546378 | 542 | |
| AA438290 | 561 | |
| AA820520 | 618 | |
| AA941597 | 593 | |
| AI455870 | 551 | |
| AA950277 | 547 | |
| AA941028 | 498 | |
| AA951077 | 247 | |
| AA951083 | 171 | |
| AA949900 | 512 | |
| AA541065 | 700 | |
| AA441093 | 597 | |
| dTPR2 (GH09432) GenBank submit | 2141 | T G T T C T T T C T T G G A T T T T T T T T T C G G C A A C A T T A A T A A A T C A T G G G A G A T |

| Accession | Length | GC Content (%) |
|--------------------------------|--------|----------------|
| AI156052 | 580 | 58.8 |
| AA391402 | 654 | 65.3 |
| AI514849 | 632 | 63.1 |
| AI519786 | 562 | 56.1 |
| AI546378 | 542 | 54.1 |
| AA438290 | 561 | 56.0 |
| AA820520 | 618 | 61.7 |
| AA941597 | 583 | 58.2 |
| AI455870 | 551 | 55.0 |
| AA950277 | 547 | 54.6 |
| AA941028 | 488 | 48.7 |
| AA951077 | 247 | 24.6 |
| AA951083 | 171 | 17.0 |
| AA949900 | 512 | 51.1 |
| AA541065 | 700 | 69.9 |
| AA441093 | 597 | 59.6 |
| dTPP2 (GH09432) GenBank submit | 2191 | 22.9 |

ClustalW Formatted Alignments

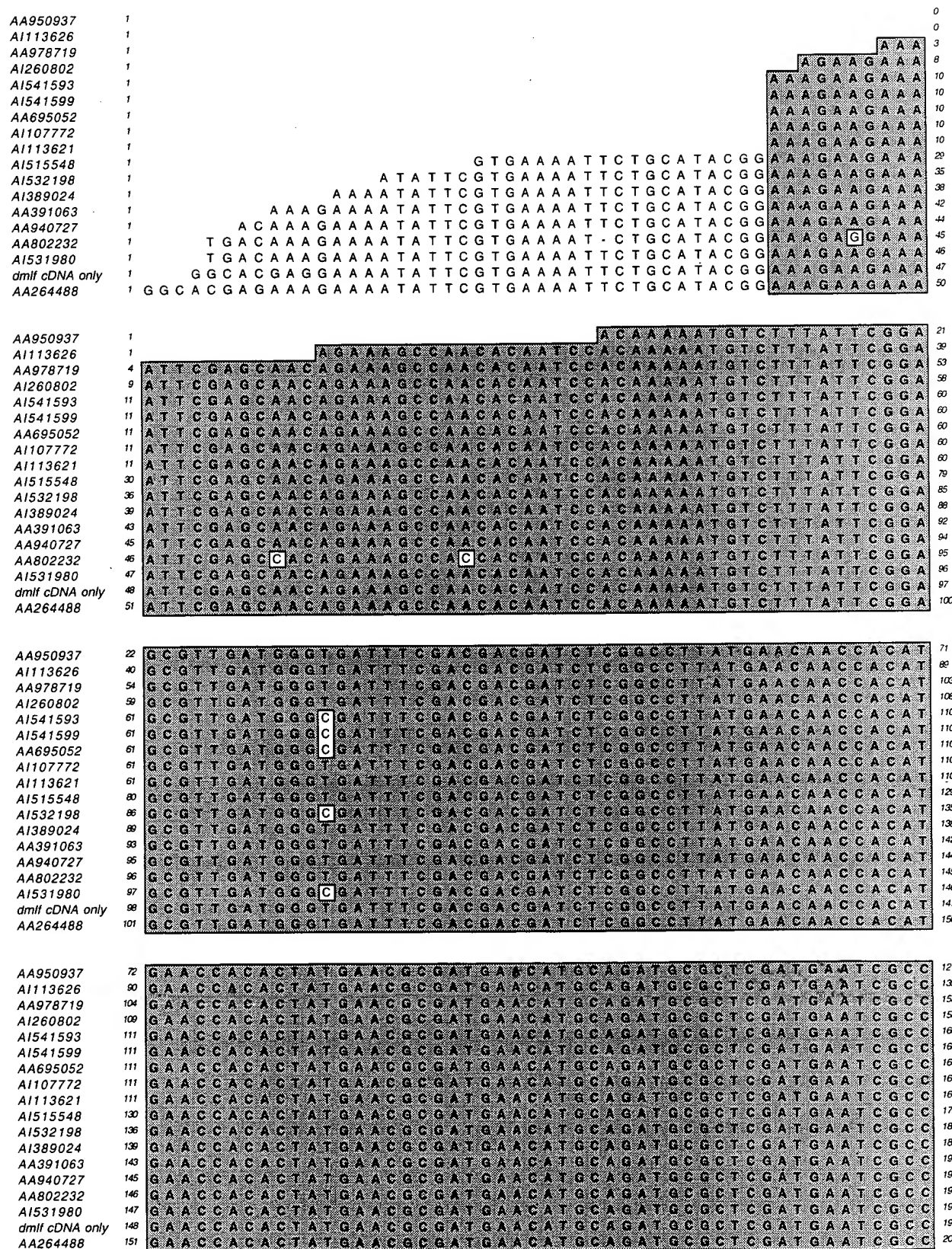


FIGURE 12 (Continued)

| | | | |
|---------------|-----|--|-----|
| AA950937 | 122 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 171 |
| AI113626 | 140 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 189 |
| AA978719 | 154 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 203 |
| AI260802 | 159 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 208 |
| AI541593 | 161 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 210 |
| AI541599 | 161 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 210 |
| AA695052 | 161 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 210 |
| AI107772 | 161 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 210 |
| AI113621 | 161 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 210 |
| AI515548 | 180 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 229 |
| AI532198 | 186 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 235 |
| AI389024 | 189 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 238 |
| AA391063 | 193 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 242 |
| AA940727 | 195 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 244 |
| AA802232 | 196 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 245 |
| AI531980 | 197 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 246 |
| dmf cDNA only | 198 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 247 |
| AA264488 | 201 | TGATGAACAGCTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGAC | 250 |

| | | | | |
|---------------|-----|----------------|-------------------------------------|-----|
| AA950937 | 172 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 220 |
| AI113626 | 190 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 238 |
| AA978719 | 204 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 252 |
| AI260802 | 209 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 257 |
| AI541593 | 211 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 259 |
| AI541599 | 211 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 259 |
| AA695052 | 211 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 259 |
| AI107772 | 211 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 259 |
| AI113621 | 211 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 259 |
| AI515548 | 230 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 278 |
| AI532198 | 236 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 284 |
| AI389024 | 239 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 287 |
| AA391063 | 243 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 292 |
| AA940727 | 245 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 293 |
| AA802232 | 246 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 294 |
| AI531980 | 247 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 295 |
| dmf cDNA only | 248 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 296 |
| AA264488 | 251 | CAGGGATTCCAGCA | GAACGCTCTCATGGAGCGTCCGCAGATGCCGGCCA | 298 |

| | | | | | | |
|---------------|-----|-------------------------------|-----------|----|----------|-----|
| AA950937 | 221 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | CA | AACTTTAA | 268 |
| AI113626 | 239 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 284 |
| AA978719 | 253 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 298 |
| AI260802 | 258 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 303 |
| AI541593 | 260 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 305 |
| AI541599 | 260 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 305 |
| AA695052 | 260 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 305 |
| AI107772 | 260 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 305 |
| AI113621 | 260 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 305 |
| AI515548 | 279 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 324 |
| AI532198 | 285 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 330 |
| AI389024 | 288 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 333 |
| AA391063 | 293 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 335 |
| AA940727 | 294 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 338 |
| AA802232 | 295 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 340 |
| AI531980 | 296 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 341 |
| dmf cDNA only | 297 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 342 |
| AA264488 | 299 | TGCCAGCCATGGGCTCTTCGGCATGCCCA | TGATGCCCA | | AACTTTAA | 343 |

| | | | |
|---------------|-----|--|-----|
| AA950937 | 269 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 318 |
| AI113626 | 285 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 334 |
| AA978719 | 299 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 348 |
| AI260802 | 304 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 353 |
| AI541593 | 306 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 355 |
| AI541599 | 306 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 355 |
| AA695052 | 306 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 355 |
| AI107772 | 306 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 355 |
| AI113621 | 306 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 355 |
| AI515548 | 325 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 374 |
| AI532198 | 331 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 380 |
| AI389024 | 334 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 383 |
| AA391063 | 336 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 385 |
| AA940727 | 340 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 389 |
| AA802232 | 341 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 390 |
| AI531980 | 342 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 391 |
| dmf cDNA only | 343 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 392 |
| AA264488 | 344 | TCGCCCTGTTGAACGCTGATATTGGTGGCAATTCAAGGCGCATCCTTCTGCC | 393 |

| Year | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| Population | 1.0 | 1.1 | 1.2 | 1.3 | 1.4 | 1.5 | 1.6 | 1.7 | 1.8 | 1.9 | 2.0 | 2.1 | 2.2 | 2.3 | 2.4 | 2.5 | 2.6 | 2.7 | 2.8 | 2.9 | 3.0 | 3.1 | 3.2 | 3.3 | 3.4 | 3.5 | 3.6 | 3.7 | 3.8 | 3.9 | 4.0 | 4.1 | 4.2 | 4.3 | 4.4 | 4.5 | 4.6 | 4.7 | 4.8 | 4.9 | 5.0 | 5.1 | 5.2 | 5.3 | 5.4 | 5.5 | 5.6 | 5.7 | 5.8 | 5.9 | 6.0 | 6.1 | 6.2 | 6.3 | 6.4 | 6.5 | 6.6 | 6.7 | 6.8 | 6.9 | 7.0 | 7.1 | 7.2 | 7.3 | 7.4 | 7.5 | 7.6 | 7.7 | 7.8 | 7.9 | 8.0 | 8.1 | 8.2 | 8.3 | 8.4 | 8.5 | 8.6 | 8.7 | 8.8 | 8.9 | 9.0 | 9.1 | 9.2 | 9.3 | 9.4 | 9.5 | 9.6 | 9.7 | 9.8 | 9.9 | 10.0 | 10.1 | 10.2 | 10.3 | 10.4 | 10.5 | 10.6 | 10.7 | 10.8 | 10.9 | 11.0 | 11.1 | 11.2 | 11.3 | 11.4 | 11.5 | 11.6 | 11.7 | 11.8 | 11.9 | 12.0 | 12.1 | 12.2 | 12.3 | 12.4 | 12.5 | 12.6 | 12.7 | 12.8 | 12.9 | 13.0 | 13.1 | 13.2 | 13.3 | 13.4 | 13.5 | 13.6 | 13.7 | 13.8 | 13.9 | 14.0 | 14.1 | 14.2 | 14.3 | 14.4 | 14.5 | 14.6 | 14.7 | 14.8 | 14.9 | 15.0 | 15.1 | 15.2 | 15.3 | 15.4 | 15.5 | 15.6 | 15.7 | 15.8 | 15.9 | 16.0 | 16.1 | 16.2 | 16.3 | 16.4 | 16.5 | 16.6 | 16.7 | 16.8 | 16.9 | 17.0 | 17.1 | 17.2 | 17.3 | 17.4 | 17.5 | 17.6 | 17.7 | 17.8 | 17.9 | 18.0 | 18.1 | 18.2 | 18.3 | 18.4 | 18.5 | 18.6 | 18.7 | 18.8 | 18.9 | 19.0 | 19.1 | 19.2 | 19.3 | 19.4 | 19.5 | 19.6 | 19.7 | 19.8 | 19.9 | 20.0 | 20.1 | 20.2 | 20.3 | 20.4 | 20.5 | 20.6 | 20.7 | 20.8 | 20.9 | 21.0 | 21.1 | 21.2 | 21.3 | 21.4 | 21.5 | 21.6 | 21.7 | 21.8 | 21.9 | 22.0 | 22.1 | 22.2 | 22.3 | 22.4 | 22.5 | 22.6 | 22.7 | 22.8 | 22.9 | 23.0 | 23.1 | 23.2 | 23.3 | 23.4 | 23.5 | 23.6 | 23.7 | 23.8 | 23.9 | 24.0 | 24.1 | 24.2 | 24.3 | 24.4 | 24.5 | 24.6 | 24.7 | 24.8 | 24.9 | 25.0 | 25.1 | 25.2 | 25.3 | 25.4 | 25.5 | 25.6 | 25.7 | 25.8 | 25.9 | 26.0 | 26.1 | 26.2 | 26.3 | 26.4 | 26.5 | 26.6 | 26.7 | 26.8 | 26.9 | 27.0 | 27.1 | 27.2 | 27.3 | 27.4 | 27.5 | 27.6 | 27.7 | 27.8 | 27.9 | 28.0 | 28.1 | 28.2 | 28.3 | 28.4 | 28.5 | 28.6 | 28.7 | 28.8 | 28.9 | 29.0 | 29.1 | 29.2 | 29.3 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|
| AA950937 | 468 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 517 |
| A1113626 | 484 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 533 |
| AA978719 | 498 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 547 |
| A1260802 | 503 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 552 |
| A1541593 | 505 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 554 |
| A1541599 | 505 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 554 |
| AA695052 | 505 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 554 |
| A1107772 | 505 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 554 |
| A1113621 | 505 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 554 |
| A1515548 | 524 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 573 |
| A1532198 | 498 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 497 |
| A1389024 | 533 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 582 |
| AA391063 | 530 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 540 |
| AA940727 | 539 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | G | C | G | G | G | C | A | C | A | C | A | T | T | A | T | T | G | A | G | A | A | G | A | G | C | A | G | G | A | C | A | T | 588 |
| AA802232 | 540 | G | G | T | C | A | T | C | A | C | A | T | C | G | G | C | G | A | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

FIGURE 12 (Continued)

| | | | |
|----------------|-----|--|-----|
| AA950937 | 518 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 567 |
| AI113626 | 534 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 563 |
| AA978719 | 548 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 597 |
| AI260802 | 553 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 602 |
| AI541593 | 555 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 599 |
| AI541599 | 555 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 604 |
| AA695052 | 555 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 585 |
| AI107772 | 555 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 591 |
| AI113621 | 555 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 604 |
| AI515548 | 574 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 623 |
| AI532198 | 498 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 497 |
| AI389024 | 583 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 632 |
| AA391063 | 541 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 540 |
| AA940727 | 589 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 638 |
| AA802232 | 590 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 639 |
| AI531980 | 591 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 627 |
| dmlf cDNA only | 592 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 641 |
| AA264488 | 594 | GCGCTCAGGACAACCTGGAGGAGCGCCAGGAGTTCATTAAATCTGGAGGAGG | 643 |

| | | | |
|----------------|-----|--|-----|
| AA950937 | 558 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 617 |
| AI113626 | 564 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 563 |
| AA978719 | 598 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 647 |
| AI260802 | 603 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 652 |
| AI541593 | 600 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 599 |
| AI541599 | 605 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 606 |
| AA695052 | 585 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 585 |
| AI107772 | 592 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 591 |
| AI113621 | 605 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 654 |
| AI515548 | 624 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 673 |
| AI532198 | 498 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 497 |
| AI389024 | 633 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 682 |
| AA391063 | 541 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 540 |
| AA940727 | 639 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 681 |
| AA802232 | 640 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 675 |
| AI531980 | 628 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 627 |
| dmlf cDNA only | 642 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 691 |
| AA264488 | 644 | GAGAGAGCCGAGCAGTTTGACAGGAGTTTACATCGCGCGCTAGTCGCGGA | 686 |

| | | | |
|----------------|-----|--|-----|
| AA950937 | 618 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 666 |
| AI113626 | 564 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 563 |
| AA978719 | 648 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 697 |
| AI260802 | 653 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 701 |
| AI541593 | 600 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 599 |
| AI541599 | 600 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 606 |
| AA695052 | 585 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 585 |
| AI107772 | 592 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 591 |
| AI113621 | 655 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 657 |
| AI515548 | 674 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 717 |
| AI532198 | 498 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 497 |
| AI389024 | 683 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 685 |
| AA391063 | 541 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 540 |
| AA940727 | 682 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 681 |
| AA802232 | 676 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 675 |
| AI531980 | 628 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 627 |
| dmlf cDNA only | 682 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 741 |
| AA264488 | 687 | GCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAGGCCATCATGCCCGC | 686 |

| | | | |
|----------------|-----|--|-----|
| AA950937 | 667 | C | 667 |
| AI113626 | 564 | C | 563 |
| AA978719 | 698 | CCGTCCAGCGGCACACACCTCGACGTTGACCATTGAGCCAGTGGAGGACG | 747 |
| AI260802 | 702 | CCGTCCA | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 600 | | 606 |
| AA695052 | 585 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmlf cDNA only | 742 | CCGTCCAGCGGCACACACCTCGACGTTGACCATTGAGCCAGTGGAGGACG | 791 |
| AA264488 | 687 | | 686 |

CCGTCCAGCGGCACACACCTCGACGTTGACCATTGAGCCAGTGGAGGACG

FIGURE 12 (Continued)

| | | | |
|----------------|-----|---|-----|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 748 | A C G A C G A C G A T G A T G C | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmlf cDNA only | 792 | A C G A C G A C G A T G A T G A C T G T G T A A T C C A G G A G C A G C A A C C G G T T C G C | 841 |
| AA264488 | 687 | | 686 |

| | | | |
|----------------|-----|---|-----|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmlf cDNA only | 842 | T C C T C C G C G G G C C G C C A T T A T T C C A G T G C G C C A A C G G C A C C G C A G A A C A G | 891 |
| AA264488 | 687 | | 686 |

| | | | |
|----------------|-----|---|-----|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmlf cDNA only | 892 | A T A T A A T T A C T A A A T C T A A A G T C A A T A C A G T A T A T T T T A C T A A C T A T C C G | 941 |
| AA264488 | 687 | | 686 |

| | | | |
|----------------|-----|---|-----|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmlf cDNA only | 942 | A T A A A A C A G A A A C A G A A T T G C A T A C T A T A A A T T T C T G C T A A T T A C A T T C C | 991 |
| AA264488 | 687 | | 686 |

FIGURE 12 (Continued)

| | | | |
|---------------|-----|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 992 | C A A C T G C G T T C A A A C G A A A C G A A T A T C G A A T C G A A A T C A T A G A A T G C A C A | 1041 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1042 | G A G C A G C A T A C A T C C A C A T C C C T A T G C C G C C A A T C C G A G G C G C C A A C A A C | 1091 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1082 | G T G C C G T A A A A C A T T T T C A C A C G G A G G A C G A A G C G G C C A G C T C C T A C A A G | 1141 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1142 | G C G G T C A A G C G C G G C A A G A A G A G T A G T A G A A A C G T G A T C A T C T G T A T G C | 1191 |
| AA264488 | 687 | | 686 |

FIGURE 12 (Continued)

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 582 | | 581 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1192 | C A A C A T C T T C C G C A T C G C A C A C T C A A A A C A C T A G G A A G C A A A G C G T T G G | 1241 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 582 | | 581 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1242 | G T T C T G T T C C A T A G C A G G A A A C C A A T T C A A A T A T T T T T T A A C A A A C A C A | 1291 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 582 | | 581 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1292 | A T T C T T T A C C A G T T C T G T C T T A T C C T G C G T G A G T C G A C C A G A A T G C A A C A | 1341 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 582 | | 581 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1342 | C T A A A A A A T G T A C A A C T T C A A G A T G C T A T T G A T G T G C A C G C A G G A T A C A G | 1391 |
| AA264488 | 687 | | 686 |

FIGURE 12 (Continued)

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1392 | A A C A A C T T G C T T A A A T T T A C T T A A A C A A A T G T G A C T A T T C A A C G C C G A A | 1441 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1442 | A T C A T T A C A A C A C A C A C T C T C A G A C C T A A T C G A A A A A T T C A A T G A A A G T A | 1491 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1492 | A T G G A A T A T A T A T G A A A T C G T A A T T A T A A G T T T G A A T T A T T T G A T T A A T T | 1541 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 586 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1542 | C T C A A G T T T T T A G A T T T T G T T A G C C A C T A A G C T T T A A A T T A T G G A T G C C A | 1591 |
| AA264488 | 687 | | 686 |

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FIGURE 12 (Continued)

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 596 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1592 | G T T A G C G T G C A A A T G A A C A C A A T T G A T T T G A A G G C T C C G A A C G A T A G A A A | 1641 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 596 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1642 | A C A A C A A T T A C C A A T T C C C C A A A T A C A T G T A A T T C G T A A G G C C T A A G T A A | 1681 |
| AA264488 | 687 | | 686 |

| | | | |
|---------------|------|---|------|
| AA950937 | 668 | | 667 |
| AI113626 | 564 | | 563 |
| AA978719 | 764 | | 763 |
| AI260802 | 709 | | 708 |
| AI541593 | 600 | | 599 |
| AI541599 | 609 | | 608 |
| AA695052 | 596 | | 585 |
| AI107772 | 592 | | 591 |
| AI113621 | 658 | | 657 |
| AI515548 | 718 | | 717 |
| AI532198 | 498 | | 497 |
| AI389024 | 686 | | 685 |
| AA391063 | 541 | | 540 |
| AA940727 | 682 | | 681 |
| AA802232 | 676 | | 675 |
| AI531980 | 628 | | 627 |
| dmf cDNA only | 1692 | A T G T T A A C G T G A A T T T A A T T A A A T G G T A A T T A C A T T A T A A T A G T A A A A A A | 1741 |
| AA264488 | 687 | | 686 |

| | | |
|---------------|------|-------------------------------|
| AA950937 | 668 | 667 |
| AI113626 | 564 | 563 |
| AA978719 | 764 | 763 |
| AI260802 | 709 | 708 |
| AI541593 | 600 | 599 |
| AI541599 | 609 | 608 |
| AA695052 | 596 | 585 |
| AI107772 | 592 | 591 |
| AI113621 | 658 | 657 |
| AI515548 | 718 | 717 |
| AI532198 | 498 | 497 |
| AI389024 | 686 | 685 |
| AA391063 | 541 | 540 |
| AA940727 | 682 | 681 |
| AA802232 | 676 | 675 |
| AI531980 | 628 | 627 |
| dmf cDNA only | 1742 | A A A A A A A A A A A A A A A |
| AA264488 | 687 | 686 |

FIGURE 13A

hTPR2 Protein 484 amino acids

MAATEPELLDDQEAKREAETFKEQGNAYYAKKDYNEAYNYITKAIDMCPKNA
SYYGNRAATLMMLGRFREALGDAQSVRLDDSFVRGHLREGKCHLSLGNAMA
ACRSFQRALELDHKNAQAQQEFKNANAVMEYEKIAETDFEKRDFRKVVFCMDR
ALEFAPACHRFKILKAECCLAMLGRYPEAQSVASDILRMDSTNADALYVRGLCLY
YEDCIEKAVQFFVQALRMAPDHEKACIACRNAKALKAKKEDGNKAFKEGNYKL
AYELYTEALGIDPNNIKTNAKLYCNRGTVNSKLRKLDDAIEDCTNAVKLDDTYI
KAYLRRAQCYMDTEQYEEAVRDYEVYQTEKTEHKQLLKNAQLELKSKSRK
DYYKILGVDKNASEDEIKKAYRKRALMHHPDRHSGASAEVQKEEEKKFKEVGE
AFTILSDPKKKTRYDSGQDLDEEGMNMGDFDPNNIFKAFFGGPGGFSFEASGPGN
FFFQFG

FIGURE 13B

hTPR2 cDNA 1756 base pairs

CGGCTGCCGCGGAGTGCGATGTGGTAATGGCGGCGACCGAGCCGGAGCTGCT
CGACGACCAAGAGGCGAAGAGGGAAGCAGAGACTTTCAAGGAACAAGGAAA
TGCATACTATGCCAAGAAAGATTACAATGAAGCTTATAATTATTATACAAAA
GCCATAGATATGTGTCCTAAAAATGCTAGCTATTATGGTAATCGAGCAGCCA
CCTTGATGATGCTTGGAAGGTTCCGGGAAGCTCTTGGAGATGCACAACAGTC
AGTGAGGTTGGATGACAGTTTTGTCCGGGGACATCTACGAGAGGGCAAGTGC
CACCTCTCTCTGGGGAATGCCATGGCAGCATGTGCGCAGCTTCCAGAGAGCCC
TAGAACTGGATCATAAAAAATGCTCAGGCACAACAAGAGTTCAAGAATGCTAA
TGCAGTCATGGAATATGAGAAAATAGCAGAAACAGATTTTGAGAAGCGAGA
TTTTTCGGAAGGTTGTTTTCTGCATGGACCGTGCCCTAGAATTTGCCCTGCCT
GCCATCGCTTCAAATCCTCAAGGCAGAATGTTTAGCAATGCTGGGTGCTTAT
CCGGAAGCACAGTCTGTGGCTAGTGACATTCTACGAATGGATTCCACCAATG
CAGATGCTCTGTATGTACGAGGTCTTTGCCTTTATTACGAAGATTGTATTGAG
AAGGCAGTTCAGTTTTTCGTACAGGCTCTCAGGATGGCTCCTGACCACGAGA
AGGCCTGCATTGCCTGCAGAAATGCCAAAGCACTCAAAGCAAAGAAAGAAG
ATGGGAATAAAGCATTAAAGGAAGGAAATTACAACTAGCATATGAACTGTA
CACAGAAGCCCTGGGGATAGACCCCAACAATATAAAAACAAATGCTAACTC
TACTGTAATCGGGGTACGGTTAATTCCAAGCTTAGGAACTAGATGATGCAA
TAGAAGACTGCACAAATGCAGTGAAGCTTGATGACACTTACATAAAAGCCTA
CTTGAGAAGAGCTCAGTGTTACATGGACACAGAACAGTATGAAGAAGCAGTA
CGAGACTATGAAAAAGTATACCAGACAGAGAAAACAAAAGAACACAAACAG
CTCCTAAAAAATGCGCAGCTGGAAGTGAAGAAGAGTAAGAGGAAAGATTAC
TACAAGATTCTAGGAGTGGACAAGAATGCCTCTGAGGACGAGATCAAGAAA
GCTTATCGGAAACGGGCCTTGATGCACCATCCAGATCGGCATAGTGGAGCCA
GTGCTGAGGTTCAAGAAGGAGGAGGAGAAGAAGTTCAAGGAAGTTGGAGAGG
CCTTTACTATCCTCTCTGATCCCAAGAAAAAGACTCGCTATGACAGTGGACAG
GACCTAGATGAGGAGGGCATGAATATGGGTGATTTTGATCCAAACAATATCT
TCAAGGCATTCTTTGGCGGTCTGGCGGCTTCAGCTTTGAAGCATCTGGTCCA
GGGAATTTCTTTTTTCAATTTGGCTAATGAAGGGCAACCACCCAGAACCCAG
AAAATGCAGATTCAGTCTTAACTTGAATGTGGAAACAGTTCACCTCCTC
CCTTCATCACGTCTCCGTGTGCTTAGAGCAGTTTCGTTTTCTCAGTTGGATGCC
CTGTGTCTCTGTGAGTGGGGTGGAGCAAAGGGAACCAATGCCGAAGACCGAG
GGCAGGGGAGGGAGGCGGGGGTGGACAGGGAGGCAGCTTGTGAATTTTTGT
TTTACTGTTTAACTTTATTAAAAAAGAAAAAAAAAAAAAAAAA

FIGURE 14 A

hMLF Protein 268 amino acids

MFRMLNSSFEDDPFFSEILAHRENMRQMIRSFSEPFGRDLLSISDGRGRAHNRRG
HNDGEDSLTHTDVSSFQTMQMVSNMRNYMQKLERNFGQLSVDPNGHSFCSSS
VMTYSKIGDEPPKVFQASTQTRRAPGGIKETRKAMRDSDSGLEKMAIGHHHDR
AHVIKKSKNKKTGDEEVNQEFINMNESDAHAFDEEWQSEVLKYKPGRHNLGNT
RMRSVGHENPGSRELKRREKPQQSPAIEHGRRSNVLGDKLHIKGSSSVKSNKK

FIGURE 14B

hMLF cDNA 1116 base pairs

GTTATGTGTTCCCGTCCGTACTGGAGGCTAGCTCTTGTCGCGGCCGCGGCGAG
TTAACATCGTTTTTCCAATCTGTCCGCGGCTGCCGCCACCCAAGACAGAGCCA
GAATGTTCAAGGATGCTGAACAGCAGTTTTTGAGGATGACCCCTTCTTCTCTGAG
TCCATTCTTGCACACCGAGAAAATATGCGACAGATGATAAGAAGTTTTTCTG
AACCCCTTTGGAAGAGACTTGCTCAGTATCTCTGATGGTAGAGGGAGAGCTCA
TAATCGTAGAGGACATAATGATGGTGAAGATTCTTTGACTCATACAGATGTC
AGCTCTTTCAGACCATGGACCAAATGGTGTCAAATATGAGAACTATATGC
AGAAATTAGAAAGAAACTTCGGTCAACTTTTCAAGTGGATCCAAATGGACATTC
ATTTTGTTCTTCTCAGTTATGACTTATTCCAAAATAGGAGATGAACCGCCAA
AGGTTTTTCAGGCCTCAACTCAAACTCGTCGAGCTCCAGGAGGAATAAAGGA
AACCAGGAAAGCAATGAGAGATTCTGACAGTGGACTAGAAAAAATGGCTAT
TGGTCATCATATCCATGACCGAGCTCATGTCATTAAAAAGTCAAAGAACAAG
AAGACTGGAGATGAAGAGGTCAACCAGGAGTTCATCAATATGAATGAAAGC
GATGCTCATGCTTTTGATGAGGAGTGGCAAAGTGAGGTTTTGAAGTACAAAC
CAGGACGACACAATCTAGGAAACACTAGAATGAGAAGTGTTGGCCATGAGA
ATCCTGGCTCCCGAGAACTTAAAAGAAGGGAGAAACCTCAACAAAGTCCAGC
CATTGAACATGGAAGGAGATCAAATGTTTTGGGGGACAACTCCACATCAAA
GGCTCATCTGTGAAAAGCAACAAAAAATAAATAGCCATGCATTTGATTTGTT
TAGTTTTGATTGTTTTAACAGTTAGTAATGGTGCTGGGTAATAAGCATAAGAC
CAATCTCTTGCTGTAAATCAGTTCTGTCCTTGGCAACTTTCTTCTGATATCTG
AATGTTTCATGAAGGTCCTAGCTTTATATTGTCCCTCTTTTAGGAATAAAATTTT
GATTTTCAACAAAAAAA

FIGURE 15

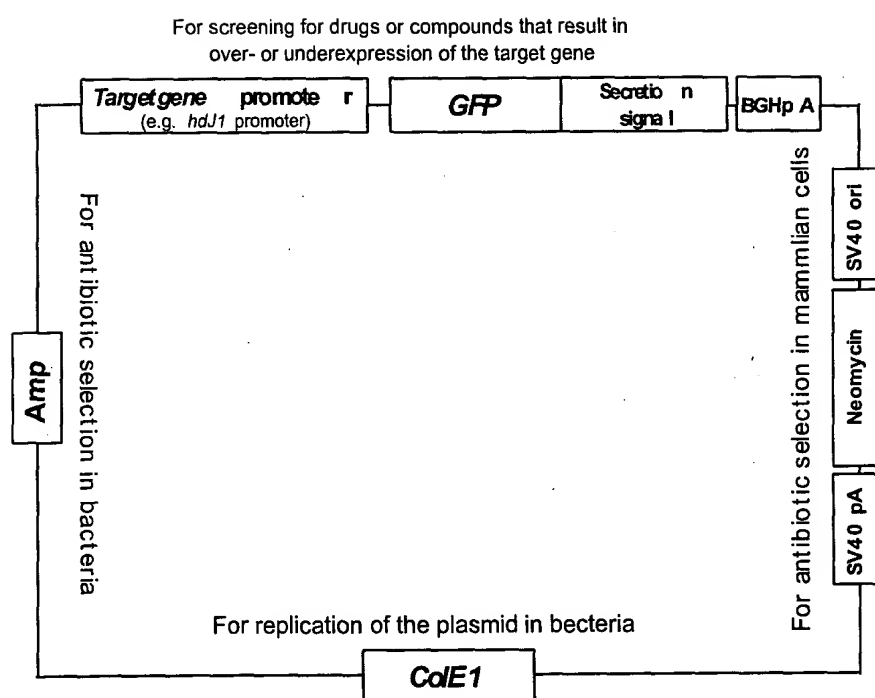


FIGURE 16

dHDJ1 5' region, 24333 base pairs

TTACGGTTTATTTACTATTACTCTAGTTAATCAAATAAACTGTATAATTCCTGG
CTTGTACAATAATTTTGCTAACACGCCGATGCGTTCGATCTTTTTTTTTTACCGC
TCTCCGTCGTATTCATCATGGTACATATTACATCCAACATACTTTATTTTTTT
GGGTATTAAACATTGGCAATATCGCTGCTCGCCGCCGTTTCGGTTATGCTCTAT
AAATAAAAGGGGGGCGCCGCTAAAATTATAATAAAATTTTCATGGGTCCTAA
ATCTAGTCTCGAAATCTATGTACAAAGTTTGCTTGCATGCTGGTTAGGCATAG
GTTCTTAACGTATTATTGGGTTGCTTTATTTCCATTCTGCGCAGTTGTGCAGCC
TGTTTAGTGTTTGCTTTACGGGGTTAACATTTTTTAAAAATGAAACATTAGA
GCGGTAACCTTGTTGTCTGATTATTGGCGTCATTAAAGCGGTATCGCCAGCAC
GCGATTGATGCAAGGATACCGATTCAATGAAATAAAAACGAATTCAGCCAAA
CACAATCTTTCATTTCTTTTTTTTTATCGTACTTAATGATAGCCTTAGTTTCTA
ATGGGACTGTGTGCTTCGGTGAAGGTTGGGGATGATTTTGGGAGGCAACAAT
TATGTTCTAGCTTATAGCTTACAGTCCTACGCCTACTCCTATTTCTAATATGTT
CATCATCAGCAGTTAAAAACGTTTACAAAACCTCATGCGAAATTGAAATCCA
ATAACAAATGCACACGCCGCAGTCGCATCGGCGTCATCTCTTCTCCTGACCC
TCGCCTATCCGCATCCAGTTAGGTTTGCTGCTGCTGCTGCGCCGACGGTTGTC
GCCGACTGAAGCCACCGCCGGCGGACAGATGTCGTTGCAGGGCTCGCTGCTG
CTGGAACCTTGGCGCTGCCTGGTCTCCGAAGCGGTTGAACTTGAACCTGTTGC
GCTGCTGGAAGTTCTGGCGATAGTTCTGATTGTAGAATCGCGGAAATCCTCCA
CCTCCGCCGTTCTTGTTCCAGCGCTTCTGGCCCTCGTACTCCTGGAATGGATT
GTACCCGGGCGTGCTGTTGCTGGCATTGTTTCCCTTAGCCGAACCGGACTTCA
CCTTCCGCTGACGTCCACGATCCATCTCGTTCTCTTCGTCGTCGTCGATGTCCC
GCTGCCGCTGCTCACGCGCATCCACCAGTAGCTACGGAACAGAAATATCAA
GCATTAGGCTAGAGTTCGGACCTTGTGAATGGGGAGGCTTGGCTGGCTGGCT
GACGCATGCGCTAGTTAATGGAGCTTATGCAGATGAGTACGGTCGCTCGCGA
ACAAGCACTGGGAATATGCACATTGTATTCGAAATGGGTGAGTGGCTTACGG
TTCACGGTTCCTGTAACAGGTTATCAGGCAAAACGGTAACGGCACAACGGT
TGAATTTATGGCGTATCAGGCGGTTGAAATGAAAGAAACAACGTGCCGGCCA
GCAGTCAAATCATAAGCTTCATTGCACGGGAAACGGATGCGGAGTCATCGG
GTGAATTACCTAGGCTCCGGTGCAGTCACTCTCTCCCGCAATGACTTTTGCAA
CTCTCTCTACACTTTTACGCTCGCTGAACGGAGGACGCGTTGTGGTGACCGC
CCGGTTGGGAACGGATACCAGCAACGCAGCCATCACAGACTATTCGGGGTAA
TCGTATTATTTGTATTTGTTTTGTGTGGTATGTGCTTAGTGGGGAAAAAGAAG
AAGCGTCGCTCTGCCGCCGACGCTTCTACCTCCTACCGGCCGTCCGTGAGAC
GATCCGGATCGGGTGCGTCAGCGGTCGTGTCTGTTACCGCCACTGCAATTACG
ACCACATCTTTACTGTCACTGCCACTAGTCACTGCCGCGTCGACTGCAACCGA
GCCCTCGACGATATCGCTGCCTTCCACACTGCCGTGACCAGCTATCCGTTTCG
CACAAACCAACTCAAAGTCTAAATGAATGGGGATAATGTGGAAACAAATG
CAAATTACAAACAAGTTCGTTTAGTAAATCAACTCAATCGAATTGCATTTTAT
GCAACAGCTAAGCGAACGACATAGAAAAACAAAAAAGAAGACCAAAGAGCCA
GTAAATAATAAAGAATTAGTTAAACCCGCAAAAAGAGAACCAATTTATGTA
CATTTTCATCGTATTAAGCCCGCAACTTGTTATTTTTGAAGCACAGACCCAAA
GAAAGTGTTAACCATGCATAGATTTAGTATCTACGTTAGTGACATGGTCACA
AGGGATAGATAAGCGCTTCAAGGTGAATGCCTCTCTAAACTCACCTCCTTTTC

FIGURE 16 (Continued)

GAGCTCCGCGGGCTTGCCATTCCAAGTACGACGCGGGGAGCCGTATCCACGA
TACGATTGCTTCAGCAGCTCATTGATGGTGCTCCCATTCGAGGTGGCATTGCT
CTGGTAGCCATTGCCACCCTTGGCTGCTGGTGCGACTTGAGCGCACTGCCGT
TGAGCAACTTTTGGCGCTTGGCGCCTGGCGTTGCGGGCGAGTCCGTGGAGGG
CTTGCTACTCGAGAAGGGATTGCGATGGTTCTTGTTTCGGCGTCGGAATTTTCA
CCGGCGATCCCTCCACCACCACGACGTCAACATCATCTTCGATGGCATCGAC
CTCATCGTTACGCGTAACTTTCCAGATACCCGTTTTTCGATTTGATGACCGCTG
GCGAGGGTGGCGTCTTTGGCGATGGTGGTGCTTTGCTTTGAGACTGTGATTGC
TTCTGTGGGTGCCAGCCATTCGTTAGCTGAATGCTGGGCTCCTCCTCATCGTC
GTCCTCATCACTGTCTGCGGACTTTTTTAGGCTCTTGAATATCTCGTCTATGGC
ATCAGTCTTTTGTGTTGCTGTTGTTAACGTGAACCGATGACGAGGCTGAGCCGT
TGGTGTGGCTGCCATTGGTCTTACTGTGACCATTGGTCTGGCCAGACTCTTGG
TCCGACTCGCTAGAATCCTCCCCACTTGGACGCTTGCAGGGGATTCCGGTAGAG
GCGCCTCCTCCTCCTCAGATGCTGATTTCGTAGGGCACAAGACTTTTCAGTGGC
GTTTTGACGGGAGTCTTTACTTGAATCTTTACAGGAGACTTTGCCTTAGGCTC
CGTATGATTCTCCGTCATATTGGGCATGCTCGGTAGCTGGGCTGTCGTTGGTC
TGGGCTTCATCTCATCCTCGATGTCTTCATCATCCGAGGAAATTGGCAGATAT
TGTTGCTGGTTTTATTGATTTATGGTTGCTGCTGCTGTTGCTGCTTGGGGAGGA
ACTTTTGTACCATTTCAGTGGGAGCTGAAGTAGCTTCGCCTTTAGCGTGAG
CGCCAACCAAGTGGAGGCTTCGCAGTGTCTGAAACTTTCCGGTACCCAGCTG
GAGTCCGTTCTGTGGACTTTGCTGGTTTTGTTGCTTGAAGTGGATGGCGGTTTT
CTGGGCATTTCCATTAGTGTAACCGTTTGTCTCCACCCGCCGGCAGTTGAGGAC
CAATGAAACGCGTTGGTGAAGGCGAAGACACAGTCGCCGCCGGCAGTGGCGT
TGTGCTGTGTCCGTTGGTCAAACGCACTCCATTGGGCCTGTTGGCCGCCGGAC
TGGCAGCCTGTGAGAGGTCCAGTTCGAAAAACATTATATAGGCATTTGTGTT
GCACACACTGTGCATTGCGATTGGCCGCACGTAGCTGTCTCGTCAAGTTGTAA
AAGCTGCCCGTATCCGTGGAGCCAATGGCCGTGTAGTGACCGCAGTGCTGGG
ACGCCCCCAAGTGAGTGACCATCGACACCAGGCGATAGGTGAGCGGTTGAGC
CTGAGCTGCTTGTGAACGGGCTGCGTATTTGCTCAAATCTATGCGTGACTTGA
AGGAAATCTGCTTGGTCAAGTTTGTGCGCATCATGGAGAATCGCTTCAGCTGT
ATACAAAGCGTGATTGGGGCACGCTCCAAAGAGAATTGCTTTGTGGCAGATA
CCTGCAAGCGATACGTTTAAATAAAATGAACTACAGAACAAGGTCACAAAG
ACCTACCTTCTTCTGTCATCCCTCGCACTTGTAGCCCATATCCTCTAGCCGTT
GCGAGAAAAGTGTCCCTCGAAAGCATCCTCCAAGGAGTCTGCCTTGCAGGATG
TCGAGCAACAGATCCTGGAAGTGCTGAAACGTAATGGACACATGGTTGCAGC
TCAGACAGCGCACCTCGCTGCGCAGATAGCCGCCAAAGATCTGTCCCAGCGG
CGTGGTCTCCTTAACCAACTGATCCAGCTCTTTGTAGTTACGAAACCGCATCA
AATACGCCCGCTCCATGGCCTCGACCAGGAAGCGCAGGAAGTCTGCGCATC
CTCTTGGCGACCAACGACCATGTGTTTGCAGATCTGCTTTAGCTTCGAGTAGA
TGAGGAAGGGTCTGACGGCCGACTGATTGCTTTGGGTGGCCAAAAGTGT
GGTCATGGCGCAAATGATGCAACCGCTGCCAGGTTTCGGCCACATTGCAGTCA
GCCAGATGCGCCTGCTCCGAAACGAGCCAATTGGCCAGGGCGGGTATGTGCA
GGAGCGCCTGAAGCGTTGAGTTGAGGTAGCAGGTGTTGCCACATTGATCAT
GCCCGTGCCACCTGCCATTTGCGCTCCGACTGCTTCCAGCCAATGCGTATGT
TCTCCCGCGGATAGAGGACCCTCTTCGGCTTGGGCAGCTCATTGGGATTGCTT
GTCGGATGCTGATGATTGTGGTGGTTGATGTGGTGCGACTGATTGTTCCGGGTG

FIGURE 16 (Continued)

CTCCGCTTGCTTGCGGGCGCCGTTATTGTCTGCAAAGGTAAAGAGGACGGTA
GACAGTTTAAGCACGTGCCACAGGAGAAGGCAGCAGGGAGACAGGAACAGC
TTGTAGAGCAGCCACAGGGCGAACCCGTCCACCATTATCACAGTCATAATGC
ATTTATTGGAAGAATTCCCTTCTGCAGATTAAGTCACTTGATCCGCGCTGCTA
TGAAATATAAATAAAACGAGCAGTGCTCGCTGTGGAACTGCTGACACACAA
TCGCGCTTCCATCACCTGTTTCGCAGTGTTGGAAAGGGTACACATTTGTTGTAC
CTAGGCACCGGACTGTGCAGCATTAAGATAGCTATTCTATTGAACAAAGAAA
CTTGAACACAAAGTATACGCCGAAAAAAATTTCCAGTACTAGATTTTGAAAT
ACAATTCTTTGAACATCGTTACAGAATGTGATATCACCAGATTTTATCTGAAA
ATATTTTCACAGCATCGTAATTTTCATATGTACCCTGAATATGTATCTTGCAGTT
TTGTTTGGGAAAGTGTACCAATCGAGGTA CTTATCCTGGTACACATATCTCAG
ATATTACCCAGCACTATTGTATCTTTGATAACAGCTAGCGTGTGAGCGGGATG
GCGACTGGCAGAAGAAGAAATTTAACTGATAACAGCAAGCGAATGAGAGG
GATGGCGAGTGGTGAAGCAGTCCAAGTGTCTGCTGCCGACGAATACAGTGGT
CTCGTTCTGGCGTAGGGGGTTGGGGCGGCAGTGTTGCCAACTGAATTTTGGC
GCGACCTAACAGTGGTTGTTGTAGGCCCAATGCTCCCCCTTTTATTGTCTTT
GTAAGTGTGTTTCGAGGCATTGACCAGGCCAAAAAAAAGAAAAGAAAAGAAA
AGTCGAAACATCGTGTAAACAGCTCCTGGTGCTGAGCTTTGTGTCCACTTCCTG
CTCTGTGTGAATCACTTCTGCGAGTCTGGCCTTTGTTTGTGCTCTTTTTATCAC
GCAAAAGCAGATTGCGGCGCATTTACCGCATCTAAAAAATAAAGCAAAGCC
AATAAAAGCACCGCTGGGGCTGGCCATGTGCGGGGGAAAGAGACGGA ACTA
CGGAGGGGAGCCCTCGTGCTTTTTGTCTTTTTTTCCTTCTTTCAATTTGCCGCTG
GAAATACAGCACGTTTTTTTTCCGCCACA ACTTCTGTGAATCAGAAGTTTGGA
GAGGCGGCTCTGTTGTTGCTGCTGCTGCTGCTGCTCACTTTTCCAGCTTACTCTTAC
GGCGTTGTACTTGTTTTGCTTTTTCCGCGTATTCTTTGCACTTCTGTTTACACG
TACACCACCCAAAAACGCCGTCACACACGACACACACGACGCACTCACAT
ACAGAAGCGCCTAAAAAGTACAGGTATGCTGCGCTGCCGACGTCGACTGCAC
TGCCGACAAAATGCAGGCGGAGCAATAAAAAAATATGTTTGCGGAAAAAC
ATCACACGTGATTTGTGGAGGGATATCCCAAAAGATTTGGCAAAAACAAAC
GGGACGATACATAAATACATTTAAGTATATATACATCTTATATATATAATATG
AAGATATAGCATGGA AAATTGCGCAAAAATTGCCACACAAAGAAGAAAC
ACAGACGAAGGCGCAGACGGAAAAAGCCACTTTTGCAAGCAACTTTTGGATT
TTACATTTTGTGTTGATCTTTACACAGTGTACTCACCATGTCCATTTGCGCCCAC
AAGTTTGCCTGTATTGTTTTTGCCACTAAAGCCATTGATGGCGCCTGGATTTC
CCGGCTTGATGACAATATATTTGGA CTTGAGGTTCTCCAGCACCGATTTCGTGG
TAGTTGGGCACCTCCTCGTATTCGATTTTGGCCATCAGGATGCGTTTGGCATT
GGCCACGATGTGATTTTGCAGGCTGCCGTTGGTGTCTCGCCGCTCTTGGCCT
GGTCAGTCGACGAGCCGGCGGAGGAGTTGCCGCCAAGGGATTGCGCGACGG
CTGCGTTGACGACATTCGCCGTTTCGCATACGGCCATCGAAACGGGCATGGC
GATGCTCCGGCTGGGGATTTGCGGTGGAATTTTGAACGGGTGTGAGGGGCGT
GGTGTGGCGTGTGTTGGTGGTTTTCGCCACCCAGTTAGCTAATGCACATGGGC
GTGCGATCCAAAGCAGATACTAGAGATCCTTCTGCACAGCCCACACGTCCTT
CAAACTCTCCTACTGCTCTACGCTCACTTTTCTCCTCGCCCCCTCTCTCGAACA
CTTCTTGTTTCACACACCGACTGCGACACCGACACACGCACTAACGCACTC
GGGAGCACTCTTCTTTTTCTGGCTTTTTTCGCGCTGCGATCTCGATCTGTTGGCC
TACTGAGCATTACGATTAAGAAACGTTTCGCTCACAAATTGATCTGTTTCAATT

FIGURE 16 (Continued)

TCGTGCGCGGCCAGGCATTTTAGAACGAAAAGTCTGCTTTCGAAAATAATGG
CAATTCCTTCCCTCGTGTCTTCTCCGACTGCGGATTCTCTTTTCGCTTCATTTTC
GTCATTTGGGGATGCCAACTCGCGAGTGGCCAAGTGACGCGATAGGCCTCTC
GAAATGTCCTAAAGCATTTACGATATTTACAAAAATGTATTTTCGATGTTTTC
TTAACAATAAAAAATTGGTTTAAATTTAATAAGACATTTGTTACCTTGAATAT
GTAAGCAATATCTTATTGAAAGGCTTGCAGCGACATTTTTTATTTATGCCTAC
TATTCAAGTTATAAATTTAATTTTTATAACGGTATTTTTTACACCTTATCAGCAC
ATATCGATAAGTGTGATTGGGAACGACAACCCATCGGCACAATGTTGATGCA
ATTGTTGAGCTAGCCTTCATAATTAGTCGCAATCAATCGAGCAGAATGGCTTC
ATCCACAGGTCTCCTGGTGGTGTCCAACATCAAGCACCTTGGCAAATCCCTGC
GAGCCATCGAGAAGTACGTGAATTCAGTGTACATCCACCTAAATGTGGCGGG
GTCAACGTCCACGACGTCAACAGTTCCACCGCCTCCGGTTTGGGGTTCGTCTAA
TCTCGCAGCTGTACGCCAACAGCAGCAGCTATGTGGGCAAGCAGTTGGACCT
TCGCGTCCTTGTCTCTCCCCTACGACCAGGTGCCAATGGATCCCTGAAGTTGC
GCCAGCCCGTCGACCTAATCTTCTCGGATGCACATCATCCGGAGCTGTGCGAC
AGGCTTCGCGCGGATCTTAACATCAGCAAGCCAACAATCTTCCTGGATGACT
CGGTCATCTCGGATTTAAGTGCCGAGCAGGATGACACCCAGCCGCCTAAGGT
GTATCCCTCGGTTGTCTTGGGCGGAACATTCGATCGCATCCATCTGGGACACA
AGATATTCCTCACCCAGGCTGTACTGCGCACCTGCAAGCGTTTGGTTGTGGGC
GTAACCACCTCCGCCATGACGAAGGGTAAGACGGGCATGAATTGGCAAATA
AAACGCTTATCTTAACGACCATTCTTATCGCTGTCTGCAGGAAAGACGCTGCC
GGACTTGATTTTGCCCGTGGAAGAGCGCATCGCCCGGCTAAGGGAGTTCCTG
GTGGACATAGATGATACGCTGCAGTACGAAATTGTGCCCATCGATGATCCCT
TTGGTCCCACGCAAGTGGATCCTGACCTGGACATGATTGTGGTTCAGTGC GGA
GACGTTGCGAGGAGGGCAGAAGGTCAACGAGGTACGCTCCGCTAAGCAACT
GCGCGAGCTGGAGATCTTTGTGATTGACATTGTTGAAAGCAACGTGCATGAT
GGCATCCACGAGACCAAGGTCAGCTCGAGTAACACACGCATCGATCTGCTGG
GAACCCGCTGGAGAAGGCCGGAGCCACGACCACAGCTCCCGCCGCGCCCTTA
CATTATTGGACTCACTGGCGGCATCGCATCTGGCAAGAGCAAGATGGGCGAG
AGATTGGCCAACATGGGCGCCACGTCATCGACTGCGATAAGGTGGCGCACG
ATGTTTACGAACCTGGTCAGTTGTGCTACACCCGAATTGTGCAGCACTTCGGA
CAGGGTATTGTTTCAGACGATGGTCGCATCGATCGGTCCAAGCTGGGACCCTT
GGTGTGTTGCCGATCCCAAGCAGTTGCAAGCACTCAACGGCATTGTCTGGCCG
GAACTTATTGCGGAGGTTAACAGGCGGCTGGATGCACTGCGTTCCCAGGCGG
ACGTGCCGCGTGTGGTGGTCTTGGAGGCAGCGGTGCTGCTGCGAGCGGGCTG
GGAGACCAATTGCCATGAGGTGTGGTCCATGATTGTGCCACCGGATGAGGCT
GTGCGGCGGATTATTGAGCGCAACAAGTTGAGCGAAGTGGAGGCCCAAAG
CGACTGGCCAGTCAGGTGCCCAATTCTGAGATCGTGGCCAAGTCGCATGTGA
TATTCAGTTCGCAATGGGATCACGAATTCACCCAGAAACAGGCGGAGCGTGC
GTGGAAAATGCTTACCAAGGAACTGGACTCTTACCAGAGCAGCCTTTAACCC
GATGGATATTTAGATTATCTTGTGATCCTTATTTTGTATGATTTTTTATGCAT
TTGTTGTATATTGTTTAGTTGTAAGTCCAAAGTTGAAAAGAAATGCTGGGACG
TCATTGGGGAAAAACGCTGAAAATTTCAATGGAACCTTAGTGGCTCTCGCCC
TTCTTGCCAGCCACTCGCTTGAAGTCGTTTCATCTTGGTGGTCATGATGGGGGA
ACCGATGAAGCCGATATAATCAATCTGCGTCACATCGCCACCTGACTGATTGT
TCTTCACGAAGATTTGGATGTTTTGCACATTCTGGAACCTTGACGTAGCGCAGA

FIGURE 16 (Continued)

TTCACGGGCACTCCACTCTCCAGCTCCTTCTGAGCCAGGCTGCAAAATGGATT
GAACAGTGAGAAGAGCTAAGCAGCCATAGAGAAGGCAATAGCTACCTTAGA
TCCTGCACACTGTTTCATGGACTCGGCCATGTCAAAGTCAATCGTGCGGGGCTG
GTTAATGAACAGCTTCACATCCTTGGGACCCAGGTGCGAAGGTGCCTTGAAC
TTCAAAGAGTGGATCTTCACAGCCTGATTAAGGTGATGGACAGGATGAGCT
GCTCATCGCAATCGGACTGCAGGTAGCCACCGGCGGAGGCCAGGGCGTGCTT
TAAGTTGTGGTCATCAGCTTCGTTGAGGCACTCGCACTCCTGCTTCGAAATAA
ATGTATTCAGTTCCATCTGTAAGAAGGATTAGGGATTATTTTTGGAACATTTC
CAAATACTGCACTATATTACCAATCCCTGCCCCTAATCCTCGCCCCCTCCTC
GCCACCGGATGTACCGATGTGCTCCTGGATCTTGGCCTCGAGCCCATTGACGT
CCGCACCCTGGACGCGATCGATCTTGGTCCTGTTCTGTAGAAGATGAATGTT
GGCATGGCCGAAACGCCCTGTCCAGCAGCCGTGTCCTGGCACTTGTCCACAT
CCACTTTTCAAGGAAGATGGCCTTTGGGTACTTTGTTGGAAACGTCTCGAAGATG
GGCGCAATCCGCTTGCAGGGACCACACCACGAAGCTGTGAAGTCCACCACAA
CCAATTGAATGCCCGCTTGGGCCAACTCCGCCTGGAAGTGGGACTCGTCGTT
GATCACGCGCACGGACATGGTGATAGGATTAGGTTTCTATTAATTGAGCTTTT
GTTTCGGCAGCCGAATTGGATTTAAGCAAGTAAATGTTATTATTAACGTTCAA
TGCAAATTTTTTTTGTAAAGATGACTTGTAAATATGCATTTAGTCCAAATTCGT
GCTAAGAAAAAATACCGAATGCGGTATTCCACAAGCGGTACACTGTGATGGT
ATCGATATTTTCGAGCTCTTTGACTTCCTATTTTTAGAGGGACCATTATGTGTA
ATAGAAAAAAACCGAACTTAATATTTAAACTTTTATTGAAATATTAGTGGA
TTACAATATGTAAACTATGAAATATTCTCATTGATATAGCTCAAAGTGTTA
TTTAAATTCATTTCAGTGTTTACGACTAGCAATCTACGCTTTCACGCTCATCTT
AAGCTTACCGCCCATTTGCCAGGGTTGTCAAGGCGAATGAGCGGTCCCACCA
TACACGCCACTGGAACCTTCGATACCTGCGCTGCGCCTGGCCACACGTTTCATT
ACCTCGTGGTGTTTCAGTCGGTCGCATTTTCATTAAGTCGCCATTTTAAATTT
ATTAGAGTCAAGTACAATGGCAGATGTGGAAAAGGAGCCCGAGAAGACCAT
CGCCGAGGATTTGGTGGTGACCAAGTATAAGTTGGCCGGCGAAATCGTCAAC
AGTGAGTATTCCTTGGCCGGAAACAGCGAACGCTGGCCGATTCTTGAGTCG
CTGCTACGTGGCGCTTACACAATGCACCGAATGCCGCTTTCCTTGTGCGCCA
CGCGTTGGTTAATCTGCCTATTTCTGGACTCTGTCTGCTCGTTTAATTTAGAA
ACCTCAAGGCGGTAATTGGACTCTGCGTGGTTGATGCCTCCGTCCGGGAGA
TCTGCACCCAGGGCGACAATCAGCTCACCAGGAGACCGGCAAAGTAAGTG
GTGGCCACCTGGCGGTTCATTGCGGCCAATTTTCATGTCCAATGATTAAGACTTA
CACCTTTGAGGGTTTCCCGATGGCGAGCCATGTGCTGTGCGGGCTGGGGATC
ACCTCGTGGTCGCCAGGCGCACGCGGGGACTCCAATGCTCCACGTGCCCGGC
TTGTGTGCTCTCCAAAAGGTCCCGAGGATTTACAGATTATGAGATCTGAGGA
CACACCGCGCACTATCATTGATATATAGTACAACGAACAAGCAATCTAATGC
TTTTATCGATCTTTCACAAACAGGTATACAAAAAGGAGAAAGACCTGAAGAA
GGGCATTGCCTTTCCACCTGTCTGTCCGTCAACAACGTGTGTCTGCCACTTCT
CGCCAGCCAAAAACGATGCTGACTACACGTAAAGGCCGGTGATGTGGTCAA
AATGTAAGTTGAACCTCCTATTCCACATATACCGCCACTAAATACGTAACATT
TCTTTTCTACAGCGATCTGGGTGCCACATTGATGGTTTCATTGCCGTGGCCG
CTCACACAATTGTGGTAGGCGCTGCTGCGGATCAGAAGATCAGTGGTCGCCA
GGCCGATGTCATCCTCGCCGCCTACTGGGCTGTCCAGGCTGCCTTACGTCTGC
TCAAGTCCGGCGCCAATGTGAGTCCTCCCTTACTTCTAGGTAATCCTCCGTTA

FIGURE 16 (Continued)

ATCCCTGCAAGAAACGGATTGTCTGCCGCGATTCTCCAGCGACTGAACATCTC
AACACTTGCAAAGATCAGCTGTGGCAGCTGGTAATTGCCCTGGCCTATTATTC
AGGACTGGAGGCTTCTTGTCACTTGTCCACAAGGTTATTTCTTCTGCAGGCAA
CGGATTGACTGCGCTCAAACCTCTGACACAGATCAGCTCAACACCTGCGGATA
GAAACTGTGTCAATTTCTGTGAACCTGAACAAGTTCATTCCATAGAAGTGTTCCG
TCTTTAAATTTGTCCACATCTCCAGTTTATAGATATGTCGGAATTGTAATCTGC
AGGCAACGGATTGTCTGCTGCCCTAACTCGTGGCTCAGCACAGCTCAACGTCT
GCAGAGATCAACAGTGTGCTGATTTCGTGAACCTGAACAAGTTTAGATACTTGAA
ATGTTCCGGTCTTTAAAGTTGTCCACAATCGCAATGATAATGCCGATCAGTTAT
TGTTATTTTTCGTTATCTATAGTATACTATGATATTTGATTAAAGATTAGTCAAA
GGGAATTGGAATGTTTTCTTTATCTCTGCTTTGAACTATTTCCATTTTATTTCA
TACTTAATATTTATGTTTCAATTCTGTATCCTTACAGAACTACTCCCTCACCGA
TGCAGTGCAACAAATCAGCGAGTCGTATAAGTGCAAGCCCATTGAGGGCATG
CTCAGTCACGAGCTGAAGCAGTTCAAAATTGACGGCGAGAAGACGATCATAC
AGAACCCCAGCGAGGCGCAGCGCAAGGAGCATGAGAAGTGCACCTTCGAAA
CGTACGAGGTGTATGCCATCGATGTTATCGTCAGTACCGGCGAAGGAGTGGT
TAGTAATCCATCAATAGACACTACATCTCCACTAATTTGTTTCGATGATTAAAA
ACACGCGCTTGAGGCTGACTTTGCTGGAATGCGGTGTTTGTTCGAGAGTGA
CTTGTTTTCGCTCGGCGTTTTTTTATACTAAAATGCGGCACGTGCAGACACCAAG
TTCCGGCTGGCTGTTGTCCGAAGATTGCAAGATTATGAGATCTGAGAACGCC
AAATTTAAGCTGGATCCTGGATCATCGCAGCCAGAGCATTATTGCTAACATTA
TTCGTATTCGTTGCAGGGACGCGAAAAGGACACCAAGGTCTCAATTTACAAG
AAGTCTGAGGAGAACTACATGCTCAAGATGAAGGCGTCCCGTGCTCTGCTGG
CAGAGGTGAAAACCAAGTACGGAAACATGCCATTCAACATCCGCAGCTTCGA
GGAGGAGACCAAGGCCCGCATGGGAGTTGTTGAGTTCGCTCGGCCACAAGAT
GATTGAGCCCTTCCAAGTGTGTACGAGAAGCCATGTAAGTGTGATGCATAT
TATTATTAATCCTATTCCCTATTATGCGAGTTGGCAGAACTTAATTCCGGACC
TGGTACACCTTCGGGTGCTAAGTGCAGGCCAGACATTTTGCCAGAACAAATTC
CAGGCATTGTGCTCTTCAGCAGTTGCCTCAGTGTGGCCTCTGTCTGAACATGG
CACTGTCAACAATCGTATCCAATCTATTAACCTGTTTTCTTATACTTATTAAAGT
TAATTTAGAGACTAACTAGTTTGAGCAACCTTTATAAAGTTCGAATTTTAGC
CGGAAGTAATAGCAAAGTTAAACAATCCTTTTCTTATCTTGCATTACAGCCG
AGATTGTGGCGCAGTTTAAGCACACGGTTCTGCTCATGCCTAACGGCGTCAA
CTTGGTCACCGGCATCCCATTCGAGGCGGAGAACTATGTGAGCGAGTACAGT
GTTGCGCAGGAGGAGCTCAAGGTAAGCTGCAACAATTTCTTGTATTACGA
TGCGTACTCAATGAAATCTCAACTTTTTGCAGACTCTGCTCGCGCAGCCTTTG
GGTCTGTGAAGGGCAAGGGTAAGGGCAAGAAGGCAACAGCTGGGGCGGGCG
ACAAAGGTGGAACCGGCGCCGGCCGTGGAGACCAAGGCATAGACCAGCCCG
CTGATGATGATCCGCACCGCCAAGCCATCAACGGAAACACAATGTGAACAAT
TGCGCTGCCCCAACGCTGCGCTCCACAGATTTTACTATCGAATTCGTTGCGTA
TTAGAGGACCCTTTTGACAACAGAACAGGACAGAAAGAGAAGACGGCAACAA
TTTGAGGATACATTTCCCCAGAAATCCTCCATCCATCAACAAGGCGGGCGGT
CGGTTCGGTCCCGCGCCAACCTTTACCTCTTTATTTCTTTACTATAAGCTGCCTT
CGTTTATCGGTCTGTTCAACATCATCGCAACGAAAAAGCAAAGCAAGAACTG
TCATCAAATTGTAACAATTTTAACGCTAAATGATCTTAAAATATAATTCAAGT
GAAACGTTATTAACGCTGCGTAGTAGGTATTAATAAAATTAACATTTTCTAT

FIGURE 16 (Continued)

AAAACAGCCGATAAATGCCAAACGATTTTTTCATTTATTTACTTTCCGCTGGCG
CCCAATTTTAATTCGATTTTCGATACGCTTCTCATTCTAATAAATGCACTTGCG
AGTTGTGTTTATTTTATACGTTTAATTTAGTTTTGATGTTTACATTACATTAT
ACAATTTGTAATTTAGATTTCTTGCCTTTTGTTATTTTAAATTTTACAGTCTCA
TCTTTGAACTCTTGTATTACGAAAGTTGCAAGAATAACTTCGTTATGTTAAAC
GTCACTTAGTGCTGTGCTCACTTGGCCACCCAGTTGTCCATCCCAGATCCAA
TCCCAACAAGACCAGACCAATTCGATGCCGTATACGGCGACTTTGCCCAACT
CGCTGACCTCTTCCCTTGCGTCAAACAAAATAAAGAACAACAAAAAACGCA
TTGCTGCGGATGAAGTATAGAAAACACGAGCAGCACTTGCAGACGACAAAG
ATATGTGGCCGGTGATCAAAAGAGGATCTGGGATTTAATGGTCTGCCGTGCG
TTACATACATGGTTTGGTGTACTTTTTTTTTTTTTTTGTTATGATCGCCGCGACTG
TTTTCTACTCGCCAGACTAATTATTGACATGCACGTCCATCGGTGCGGAGGCG
GTCACGTTGCTCGACTTCTCCGGAGAGTCCAGGTAAATCTTCAAGGCACGTT
CCGGCGCTGCGCATACCGCGTGGTGGACACGCAGCCACCCGATCCAGTCGT
GCCTTCTCCCTGGCGTTCATCAGGCGTCGCTCCTCCAGCGTCAGTCTCGCGC
AGGTACCGTCCTATCTCTGTTGAATTCATTGGTTAGTCTAGGAACTGAACTGC
CACTTGCTCCACGCTTACTTGTACAGGTAGATGTTTCCTGTCTGTGTGCTATTA
AGCGGATATTTGTCCAGGGTGGTGGGCACGGAGTACCAACTGCTGGACTCGT
TAACACTTAACGCTGATATGCTTGTGCAGGGGAAGTTGCTGTTCAACTGCAG
AGAAGACCAATTAGATCAATATACACAGTAGAACGCAATTTTACGAACCTTC
ATATAGCTCAGTTTGTCTATTGGGATGTCGCTGATCTGTGATAATGAAAGTCT
GATTTTCGCTGTCTCTGCAGAAGATACGAGTTCGATTTACTGCTTACAGGGCA
ATATACAGATTTAACTTACGGTCCAAAGTGATTTCTTGGAACCTTTCCAAACTC
CAGTTTAGCCGGACACCACCGTCTTACAAATAAAGTCAGAGAATCGTCCTTG
GGCTGCGGGTCCACTTCTCCTCGCACTCTTGCACAATGAACTGAAATGGTGT
GATATAAAATCCAAGTTAAGTTTTTTTTCTCATCACAGAGACAGGGGAACCCA
CCTCCGCTGCGATGCTGGAGCGCATGTGCGAGTAGAGCGTTTCATCGTCGGA
CAGAATTTTGATGGGAATACGTCCGCCCTTCAGCCAGATGCGACAGTTTTGCA
CAGACAGTGTGGCGTACTTGGCGTCTATGCGATGCAGCTTGGCCACCAGTTCC
TTCTTGGCCTGCTCCGCCGTGGTGTGGCATTGTAGACCCACTCGCATAACGCA
AGGCAGTTTGGACGTCTCGTTATCAATGTCCGCCAGTCGCAGGAAGTGAATC
TTGGCCTTGAACCTCGTCCGGCTCCAGCGTCTTACCCAACTCCACCGTCAGTGT
TTCGCCTTCTATGAGATGTACCAACGAGTTGTTCTGGTTGTTTCGACAGATTAT
TATCGTGTTCGCTGCAGTTTAAAGTGGGCGGCGGGCACTTGGATCAGCTGC
TCGATGTGTTTCTTAAAGGCCCCCATTCGCATGTGTGTGCCACCAGCAGCTT
ATAGGCACGCGTGGGCTTACGCAGCTGAGCCTCTTCGTCGGACTGGTGACCA
GAACTGGAACCGGTGCCAACCACATCCACGCACTCGACCTTTGTGGCGTAGA
AGAAGTGGTTGGTGCTGGTGGGCAGGAGCAGCGGATCCACCACATCGGCCGC
CGCATAACTGCCGTTTCCATTGCAGTAGGCATGAACGCGCATCATGGCATCGT
GTGAGGCTGCTTCGTCTCCGGACTAGACAGCTGCGGCGAGTGACTGGTGGA
ACTGACTTGGCTGTGCGCTCCACCGCGATGTGCCATGTTGTCCGTCTCCACCA
GAGTTCGGTCTCCGTGCTCAGACTACTGTCCTCCGAGTTGGACTCGTGGCCG
TGGCTGGGACTGGGTTGTGACATGGGTTCCACTAGATCTCGCTTGTAGCGCCT
CCAATCGTAGTCGTTGCTGGATGACATGTGACCAGGTGCCACGCCATTCATCA
TTGCAGCATCCACAACATACCCCCGCTGGCGCACTGAAAGGACAGCCAAAA
ATTAACCTTAGTTATAAACCCAACAGCTGTATAACCTACCTCGACTGACTCAA

FIGURE 16 (Continued)

CGGTGGGCACACCGAGCATCTCAAGGGTCGCGGCATCCGTGTTGGGTACGTT
CAAGTAGAAGTATGTTATGGACTTAAACTGGGTGTTGGCCATGTTCTGGAGA
TGTTGCAGGGCCTCCGGCGTCGGATGCGGATCGTAGGACACGAAAGCCTTCG
GCACCGTGGCGCGCACCGTGGCGAGTAGGAACTGCTGCTCGCTAATGTGCAA
ACGGAGGGCGATCGAGCGGCGAAGGACGTCGCTGGCTTCCCGCTCCCGCGCT
GCTGAGTAAACCAGGAAGGGACCGTCCATCGCCATGGTCGATAGATCTACCT
TAAACACATACCAAGTAATGCCGTTTCGGCGGATAGACCTCAAACCTCTTGGTC
CTCGGCCCGGTACTCCAGCAGGAAGTCGAGACTGTAGTTCTGCGCCGCGCGC
AGTTCGGTCAAAGCTGGGTCTGTGCAACTCTCCAGGGACTGAATAATCGTGT
CCATCGAGGAGTTGTAAGCCACCAAACGACAGCGGGAAAGCGGCGCGAATT
GTTCCACATTCAACATCTCATAGGCCGACATGAGGACCAAGTTGATGTTGAA
ACTCTGCGATACGTACACTCTGGTAATCTTCATCTTCTTCAGGGAGGGATTAT
AGAAGTAGACGCGCGGCTTGTACAAATCCGGAAGAGCCAAGTCCGTAACCGT
GATATGCCTGCCAGGCGGGACACGCGCGTCTCCTCCTCCGAGTGCAGCTTTG
GTAGCAGCGTTTTGATGTGCTCAGGAAAGTCGGCCACCTTGGCGACTAGCTC
GTTTCTTTTGGCATCCACCTGCCGGTACATCAACATGTATGCATTGGTGCTGG
AGGTGTAGGCACTGGAGTAGTAGCTCCCGTTGGGTCCGCCAAACGAACGTTG
GATGTCCTCTTGGGTGATCTATGGATAGATAGTCGTTCAATATTTTCTCAAGT
TATGAATGTGTTGCGAAAACCTACACTAGTCACGTTCTGATCGTTAAAACAG
AACCCTCGTTGTTGTGCGAAGTCCTTAATATAAGCATAGTAGTGCCGCCCGA
AGCGCTGCCTGAATGAATCATGATGGCGAACAGTTCGTAGAGATACGGACCG
GATCCTTGCTTGGCGCTCTTGCTGGTGCTGCTGCTCATGTCGATGCCTTCATCC
TCGTCGTTTACATCGTTTTTCGTGCTGACTAGAGCTCGCTGTGGTCAACACGCC
GCTGCTCAAATTATCGTCCTCCATGGCGGATCCACTATCCGCCGTGCTGCAAT
CGTCCACGGTGCCGTTGAGCTGAGAGTTTTGCTCACCGCTGTTTCCACTTCCG
TTAATGAACGTGTTTACGGTTGAGCGTCTGAGGGAAGGTCCTCTGAAATAGA
GGGCGAGCATGGAATTAATGCTTATGGATTATGGCAAAGAGACTAACCTGT
CGTTTAATTTGATGCGGTGCATGGTCTGGTAGTCAAAGTCAAAGCGTTTAAGG
TGCAGCGTGAGGATGTAGGGAAAGGACTTAAAGTGCAGTCCCTTGTGGGCGT
CGCATTTTTTCTTGCACTTCTCGCACAGATACTGGTTATTGCCATCGAGTGTTT
CGGGCTGAACGAAGGCACGCAGAGCTTCCTCGATGCTGCCGTATGCGGAGCT
GCTTCCAAAGGGCCTCACAGGGAGCGGGATATCTAGAAAGGTGTCTTCGCGC
GTCTTCTCGGTATTGCACTCCAAACACTTGACATAATCATTTCATCTTGCCCTC
GTACAGATTAGAGATGAGATTTGCCTGCTTAGTGTTCTTGAATTTGTGCTCCA
GAGCGTCGAACATAACTCGGCACAGTTCCTGGATATCGTGCTGCTGCCATGC
CTCCGTCGAGTCCCACCCAAAGCTGCGAGTCAGGTCTGTGGTTTCTACCGCCG
CTTTGGGCGAGGTCTGCAAGTTGAGGAAGAGCTTTTGCAGTTGGTATGGTAT
GTTCTTGGCCTCGTTGTGCTGTCGAACTCCCAGCGGTACAGAGCATTCTGA
ACTCGGGTGTGATAAAGAGTGCTGTCAGCAAGCTGTTTAGATAGCAGGTCAT
GGCTTGGTTGACCAAACCAACATATCCCCTGGGACCCAAAGCTCGCCTGCCTTG
CCTCTGCCTCAGTTTCTGTGGTGGCCGAGGACACGAAGTCCGCACCCGTTGTG
TTGACTCTCTGCCATGCTCGCAACTCATCGCCTCCATACTTGCGACGATAGAA
GTTTGACAGAGCCGGGTACGTACCATCGTCTGTTCCAATTGTGGATGGGTCTG
TCACTCCGGTCAACCCCTCGACGTCCGAGTCACCGGTCCGAGCTCCGTAATC
GTATCCAGGTCCCAGCATTGTGCGACTAGCAGATGCTCCGAGTGCCAGGTCTG
TCATCCGACAATTGTTTACGATCTGAGATGAAAAGATCTGAAGGAGCATCGT

FIGURE 16 (Continued)

CCACCGGTGAGATTAGGTTTCTACCTTGTGGATACAGCTGCAGTTGCTCAGAG
AGCTGTTGCTTGCTCAGGGTGTCTACTGGTTCGCAGTCCAACCTCTTTGATGGG
TGATGACGGCTTGATTGGACTCAGCAACTCTAAAGTCGGCTTAGAAGTGACC
TTGGCCGTTTTCTTGGCCACAGGACTCTCCGAAGAAGTGTTTTAGAGTTTAT
CTCTGTAGACAGCTCGGGACATTCTTCAGGGCTAGCCCTGGGAGCTTTTTCCG
AACC GGCTTGAGATCTTTGCTGCAGTCGTCTTGATCTTGGAAGTCTTTTCG
GGACTTGATTCCGAAGTATGCTGGTCTTAGCCAAAGAGTCCTCACTCGTCGT
CTTGGCCTTGCTTGAGAGGAAGATCCCGAAGCTGGCTTCTTTTTCGTTTTCT
CACCAACTACGCGTTTCTTCTTCTCGCCGGTGGCAGGACTCTTGGCCTTCTCG
CCGTCCGACTTCATAACCTTTTTGACTACCACTCTTTAATGGGTAAC TCAA
GCGTTTGGTCACGTCACCATCCCAACTGCCGGAGGGCAGCAGGATCAAGTGA
TTCTTCAGCTGGGGCTCAAAACCAGCCACTTCGTACATCAGCTGAGATTCCAG
GGCATTCAAGATTGACCTAAAGTAAAGGGGAATTCAATTAGCGGTTTATTAGA
ACCTCAAGATGTGCAGATATTTTACCAGATCCTTGTTATCGTGTGGCTGCAG
CAACAGCTCGAACTTTTCGTACGAGAAGTGC GTGCCAATAAGGTCAATCAGC
CGTTTCACCGTGAAGTGGGAGCGGACCACTACGTTGATCTTCTTTTGCTCCGA
GCCGGGTGTCTGGTCAAAGACCGAGACGGTGC ACTGCTCGCTCTCCTTGTCGG
TCATGTCCAGCCCGCGGAATAATCAAGTGATGGTGGAGAAAACCTGCAAAA
AGATTGTAGGCGAAACGTTGGCTTTACTTATGAATTTTGTCTGGAGTTTTCTTT
TTATTTTTTTTTTATTTCTTTATTTTAGAATTA AAAAGGTGACACGACACCTTG
ACGTTTTTCGGCGGGGCCAAGTTCCTGGACATGACGATGCTTCTTGCCCATAG
TAAATAAGGAAGAGATGCCAGCCCCAAATTACTGCGAAATCTTCTTGTTTTC
GACCCCATTCGCGAATAAAGCGGCAGAAACCAAGAAGATTCCGTCCACCTC
CCGCAGCCGCAGATATTGACGTGCTCCGGGTTTGCTTTTCGCGCCTTATTTGT
ACGGGCCAGCACCAGTTGCCGTATACATATATATATATATATATAGATAGAT
ATACACATATAGCACGTACACCCAATCGAGCATCGACTGCCCCCGAAATCG
ACGTCGTGACTAACGCGCAGGGGAATTTCTGTAAACAACCGGCCATCAGAGTT
GCCTCCGGAGGATGCTACGGGAATTATTATTTGCCTCCAATGGACTACCAAC
GTCATCATCATCATCATGACCATAGCTATCACCATCGGGCGTACCGAATGCAT
AAATTTCAGTGCAAATGTCGCTCCATGTTTCAGCTGGCTTCCTTTGTGGCTCC
CCGCAAGACTCTGTAACGGAAGTGGTGGCTATTATACGAACGAATATCTGGC
GCCTTCAATTCGGCAGTGCGCATATTGCAAGTGGACGGTGGACATATCCATA
TGTACAAATTAATACTTATCGGACATCAGCGTGAACACTGCGAATTATTCTAG
AAACATTTGTAGAATTCGAAAAGATTTAAGGAAAGCAGATGCTGAATATTAGG
CGAAAAGCGATTGAACTACTCTATAATATGCAGTCAAAAATATCATCGATTCT
GCCTGTCAATTAATTGTATCTAAAATTATACTTTTCGAATGTCTATTTTGGCAA
TAATCTTTAGTGATTTCGTACTGCTCAGCATTTAATTGAGTGTGCAAGCAATT
GGGGCCGGGGTATTTGCAATGTTTTTCCAATTCTCTGCACCGAAATAACCACA
AAAAAGACAGCCAGTCAGCCAAGATATTTTGGGTCTCCTCCGAATGGAGGAT
GCACATCCACGATGTGCGATGTGAATGCGCTGCAATTGGGCGTTCAAACACA
TGTTGGATGGTCCAAACACAAACCGCATTGCCCGGCAAGGGAGCGAGTGAGA
TGGGGATCCAAAAATGCTAATACAGTCGGCCAGCACAAAATCAAATAAG
AAACCCATGCTGCTAAAAATAAAAACTGGCGGCGGCGACACAACGACACAT
CGGAGCGGTTCGGA AAAAGCACACAGGCGAGTGGAGGAGCAAGATATAAGAC
AGCTTTGGGAGCGTCTTGAATACGCGTATATCTGGCTATTTGTGAATGCGAAG
GTTTTTGAGAAATTCAGAGAAGCGCACAGACTGTTTCAATACGTCTATCCTAT

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FIGURE 16 (Continued)

ACATCAGAATGGTCAGGCACTTTCAACACATTGGCCCCATCCATCCCACTCAA
TATTTACATGATGACGATGATCTTTTGGTCAATGTTTGTGTTGGTCGGGTATT
ACAGAAACCGATATCGCGAGTTATCTATGCCATATACACGATCCAATGGGGG
GACGGCGGGAGGGGCAACAGTCATGCTCGCATATATTTGTGCTATTTTTGAA
CTATTTTCGGTACTGCGAAATCTATGTGATCTACAAAAACCATGAGATGTCTGA
GATATGACTGCTGAGTGCCGAAATTGTAGGATTCTCGATTCCCGATCATATA
ATGCATTCTCGAACAGAAAATCTCCATTACGAAATGCTTTCTATTCTTAGGCG
TCGCACAACCTTTAATTGGAGCTTCCAATGTTGTGTGAATAAGTGTGTATATAT
CCGTGGTCTATATATGCAACGGATTTTGGTGAGTTTACCCTGTGTGTCGGAA
CTGAGTGTGCCGAAATCTTTCCGAAC TAGAAGACCGCACCGTCAACGCACGG
CATAGTTCACGCGTGTACTGGCCGCTTAGGATGCCGATGCCGATTCCGATTGC
GATCCGAAGATACACCACCCGATCTGGCGCCCGATCTTTGGCGAAGCGAGCT
ACGTGTAAAGTTCTCGGCGTGATGTACTATAACAATGAGAAACAGTTTACTTA
TCTGGCTTACACTTCAATAGGAAAACAATACTTTTATATAGCTTCTATAACTT
CGGGGTGCGATAAGAACATGAATACAGATACACGGATTGCAACAGTACCCA
AGCCACTTGTTTTAAACAAATAACAGGATAATGGGGAGTAATGTAAGCTATT
GACTGGGTTACAATCAGGGGTCTGATAACAATCAAACATTGTCCAGTTGCCTT
TTGCGAATATCAATGACCACTCACGAGTTGCAACTGATAACGATTATCGCCG
CACAATGCAGTGGGTGGGTATTTCACTGGGGGGAACTTTTGGGTCCCTAGAA
CCCAGACGGATTACTCAATGAATATAGGCGATATGTTTGGGTTTACAGCGAA
AGTGCTATTAATGTGACCGTATGCTCTCTTCGATGTGCCAGCTCTCTATTTGC
GGGAATGAATGACTATTTTTATGGGTCTGCCGTCGCTGCTACAATGCTGCATT
GCTGCAGTGGGACATCCTTTGAACAGGCGCCATGCCAAAGGATATTCTTTGT
GGAAGGGGGGGGGGGGGGCAAGGGTTAAGGGTCACATTTCGTTTGCGCAATAC
TTCCAGCGATGGGGCGGTGAACGGTGGGCGGGGCGATCGGTCAAGGCTTCGA
CTGTGGAACGTGACACGCATATGTGCGCCGGAGTTTGGCCCAAAAAGTGGCC
CCAATGGTTGTCCTTCGCGCTGGCAATTAGTCCCTAGCAAGGCGCGTCCATAT
TTTGCAAAAATTTCGTGGGGCGCCTTGTTTTCTTCTCTCTGTATGTGTGCATGTG
TGTGTACCTCCGTCTCACTCACCTCAAGTGTGTGTGTGTGTATGAAAATACTG
CGGTATACGGCTGCGTTTGTGTGTGAGTGTGGGTTTCGGCTCTACTCTCCCGA
TGATCCTGCTCCTCCGGTCTAATCCCGGCTGCTCGGCTGCTCCTGCGTCCT
GACTGCGCTAGAAAATTCGCTTAAAACGAGCCTCGACGGGTCATTTTTACAATT
GTTTTTTGTTGTTCCGTTCCGGTGTTTTACCAGACGTGCTCGTTCCGGTGTGAC
TGCCCCGCCGCTGACTGTAAAATACTAAACGCATTGCAGCTGTGGCAATGCCC
AAGTCTTGGTCTTACGGTCACACTGGCAAAGTTTAAAAATTTATTTATTTCAA
CTTTCAGTTACTTTTCGTTGGCTTGAATATTACACTAAGAATTCAATTTGACAC
TTGCAATTTATACATTGTATATTATAATATATTATATGTATTATATTTTATATC
ATATAAAGATATTTATATCTATTGATCTTTTGATTATAAGCTCTTTGGTTGAAC
AATATAAGTGCAACTTTCTCCATCACCTTCCTATCTTTTTACAATATGCTTACC
TCGTCAATACGTTTTTTCTATTTCAAATATTTCAATATTTCAAAGAAATATTTT
GTTTATTTTTCTGTGTGTTTTTAAGCAATCTGACCCCTGTAGAAGAATCCCTTA
TAATATTAACAAATGTATCCTCAAAATAGATCGATCTCTATCTTCGCAGACTT
ACACGAAACATTCCAGAACCGATAGTTTTATGCGATATATGAGATTTAAGGA
GTACTTTCCGCATTTCCGCATCACAGTCACGCTTTCCTTGGCATTTGCAATCA
AATAAGCGCTAATAATAATCGTAAAAGCATAAGAAGCATATAAAGAAGAGT
CACCGCCAAAAGCATGCACAAATATATATAAATGGGGAGCGATTAAAAACA

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FIGURE 17

dTPR2 5' region, 13015 base pairs

AGACAAAGACAGCGCTGACTTCAGTCGACTTTCGTATTCATTGTTAAATGACA
TGCAAATGTACGAATGACATGGCATTTCGCCAAAGGGTTTTGAAAGGGGGGCC
AGATCCAAAGGGCAGGTCTCAGGGAAATGTTTCCAGGCTAATTGTGGGTTTT
ACGCCCTGTACTTCTCCAAATGATCAAGTACGTCATTTAATGGAAGCCACTGA
CAATTGGAATCGTAAATTATACAGCACAACTAGATTTGTTTGAGTGCTCTCA
ATGTAGGCTAATATTAGATTTCTGCGCTGAATTAATAATTATTGTAATACGTAT
TATAATGCATTTGTACCCAAATTTGACAGACTTAAGCAGTTCTCTAACATAAT
TGGCATCATTGGCAAAGAGAAATAATATTAAATTGGCAGCATTGCCAGAAAA
AACTCTTCTCCTAAATTTTGCTTGATTGAATGTTGTAGTTGAGAATGTTGTAA
AATAGTGTTAGTATTGTAACACACGACATTTTCAAATATTTAAATGAAAATC
ACATGGTAATTAGCAATTTTGGGTGGCCTTCTTCTCCTCCCAAGCCAAAGCCA
TATAATTTTCAGCCAGCTACTTGCGATTTCCCCCATGACCAACAACAACAGCCC
CATATGTGCAGTGCATTAATGCAGATTTCTTGGCAATTGTTTTTGCATACTTTG
TTTTTCTCACTCACTTCAATTTCAATTGGCGTGCTAATAACTCATTTAGTTC
GCAACAAAAAACAACAAACGAACAGCGGGCCACAAAAAATGTAGCTACAA
ACATGGCACACCAACAATGGATTGGATGGCTAACCAAGATCGCCCCCACTTC
CCTTCCATCAATTGCGAATATATCGCATCTCATGATGCTGAGAGAATACTCG
TACTCAACTATGCCGACTTTATATGAACACTGTGTGCAGTTTTGTTTTAGGCTT
TGTAATTATTATAAAAAATAAATTGAACTATTGTTGCCTCATTAGATTGAACA
GTGAGGCAGCCACAATGTTGCTTTTGTTATTCGGATACACTCAATTAAGCTGA
ATTTGCAAAATGCAAAATGGCCCGTATGAAACTCACACCTCGAAAATCATAGA
CTCGAATTATTTTAGAAATTTAATAATAATTATATTTTGTTTTCTTCTTTTTTTT
GGTTTGTTTTTTTTTTTTTTTTTTGTTTTTTGTTTCTTGCAACACTTTTCCGCCTC
TCATTTTGACAGCCCGAGGAGTTCGGTTGGTTCAGTTGATCTCTTGATTGTCA
GTCAGTCATTTGTGATTAGACATTCGACAGTCGCCGCTATTGTTGGATGGCAT
AAATTATAGTCTGTCTCAACAACAAAGCGCTGCATATGAAATCCACATAATA
AATCAATGTGCTGTCGTAATTTGTGTTAAGTTATTTGTAATCAATTTGAATTCT
CGCCGTACCTCCCCACCCCTCGGTTGGTGAGATTTATGGGAATATTTTATT
CATTTTGCTATTTTGTTAAATGGCTTTTGGGGTTTTCCCGAATATAAGTTTA
AAATTAACGCGCAATAGGCTTAAGATCATGTAATATTATATATTGCCCGTA
AACAAATGCTTTCTACTTTCATTATCATGAGTGTTTTAAAACTCCACGACTGC
TCTAAACTTTAATCTTTAAATATTTTTGTACCCTTTGAAGAACTAACCACCTAG
CAAATCCCTCCTATTATTTCTCAAACCTCTTGCACTTATCGAACTCGCTTCCTT
TCCCCGCCATCTTCACTCGAACAAATTTAACAACAAATTAAACTGAAATGCA
GTCAAATCAATCGCTGACTTTTCAATTCGTTTTTCTTCTTTTTTCGGCCCAACA
TTTTCCACTTGGCCCGAGCGTTTTGCATAGTCCATGGCTTCGATTGGATCGGC
TCGGATCGGTTGGTAAGTCTTCGGCGGAGTATGGCTTTAGTCCAATTTAGTGG
AAAGGTGTGCCACACAGCTCGGTCACAACACGTTGCTGTGGCTCATTGGAGT
TTCGCCTTTGCCTCGCTGGCTTTTGAGCCGTTTGGTTCGGTGCCGCTTAAACGC
CGTTTTAGCCAAGTTAGGTGAAAAATGCCAAGGGAGTGAGGAGTGGAGACC
GAACTGTCAACTGTGATCAAAATCAATTGTTTGCCATTTGCCAAACCAAATTG
ACTGAGCCAAGTCAGTGCAGTGCACACAAAAATGCTGACAAAATTATACCAT
AACCCATGAAATGTCAAGTCAATAATTTTTGTAATTATGAGAGCATTGAGCT
TGAGTACATAAAAAAAAAGTTATATATTTAAAAAAATCATTATTTTAGTTGGC

FIGURE 17 (Continued)

TGCCATTGGAGAAGCCCCCAAAAAAGGCAAACAAATATAATAAAAAATTATT
GCAACGTAAGTTTTGATTTGAACAAAAGGCGTATACAATTGGATGAGCTCAA
GAGTGTTTTAGAGTGAAAATGTGAGGATCATTGTTGCAACCACTAACAGA
GGTTCGTCTCTAACATTTTTTCAAAAAAATTACATAACTTTTTAAATTTGATTTCA
GTTTATTTGTAAGTGAGAAGCCTATTTTCTAACCATAAATTCTGCACGTAAAG
AGTATTTCTTTTCATATCGTATCTACAAAAATCAATCCAACACACCTGTTTCA
TCTACCGTTAACACCGTTAAGCCCCGCCCATTTTCTTATCGAAAATATAGCC
CTTTTTACGCTCTATTTATAGCATTACATTCTTTCTTTTTTTTTGCACTTTTT
AGCTGGCATATCCTTTGACTTCCGCCATTGAGGCTCGCCCAATTTCCGTTT
CGAGTTTAATTAATTTAATAAACAAATTCTTTTCGCTCTAAAAACTCTCAAGT
GTATCGATACGATGCGTTTCTTTTTTCTTCGTTAAATAAATAATAACCAAA
AAAAAAAAAAAAACCAAAAAGTAGGAGGAGAAAAGTTATTGCCATAGTTTTTTT
ATTATACTTGTGTGTTTACCTTTCTGGTGGCTTGATCGATAGGCATCTGCAATT
AAAAAGAGAAGAAGAAGAGACAAGTGAGGCAAAATTGTAAACGTTTTGTG
TAAGCTTTAATACGAAAAACAAGTACTGCAACATAACGGAAGGAAACACGG
CTTAAATTCGGGGCACAAATGCTGAAAGGGAAGTTTTTCATTGACGGGTTCG
TTCTGACGGACTTGCATTTTGGCGGGCAAGCGGGTGTGAAAATGCACACGCC
CCGAGAACCCCCCTTTCCACCCCCCTGGACCCCTTATCCAGCCCACTGGCC
AAAAACAATTTGTAATTATCCACAGAGAGCGCTGCCTTCAGCGGTTTCGCATT
TCCCCTTTCGCTCGCTCTCCCAACTTGTTTCAATTTAGCGCAAAACTTTTTCAA
CCTAATAATAGGTTTAACCGCATTTTTTAACCGTTCCTCATGTTCCGGTCCGGTTC
GGTTTTCAAACCGGGAATCGTACTTAGACTGGGTCTCCTTATTTCTGTTCTG
GCTCTCTGTACAATTTTCATTGAGAAAAATGTAAGTAGTTTTTTCATAGCAAC
GGAATACAATTTAATCCAATAATCCAATAGTTTAATCCAATACAAATGATATT
ACTACCATTTCTATTTTCGTTAATTTTCGATTTGACTTATTTGGCTGGATTTACT
TTTCAAAATATATGTTATCAATAAGACACAAACCTTACTTTTCTAGCTATTAA
CATAGTTTAAAAAAAAAAAAAAAAACTAATAAAAATTACGTGAATCTAAATTTT
TAAACCCGATATCCAAGAAGATCTCAATTTTTGCCTGTGTACTCAGTTCTCTG
AACAAAGCGCATGTGCACTTTGGAGCACACTCCATACATGTGGCTCAGCCCT
TTTCATAATTAAGTAGATGGTTTTCCATCGACTTCATTGTGGTCAGCGGCCA
GTTCAACCCGTTCTTCACTGCAACCGAGAAGTGTAAACACAAAAACCCAGG
ACTCTACATTGGCTTAAAAAATAAGAACAGAACAGAACCAAAACCAAAAA
AAGAAGGGATATTGAAATACAAGGTTGTAATCGTTTTGACTGTTGATGTCTC
AATGCATGGGCAGTTCAGTTAGTAAATGTTTTTCAAATCTTTCAGGCAGGAG
ATGTTTAAATATCCATGAAATATTTGGATCTCCTGGGGATCAATCGGAATATT
AGCCTTTAATTGTGTTGATCTTTTAAGCCTTTTTGTATCTAATCTAAGCCATTC
GATCTAATCACAATTTATAAATATCTGCATATTTCTGTATAAGTCTGCATCAT
TTGACGTAAGTCTTTAAGTCTTTTGGCTTAAGTTGCAACTATAAGGAAGTATT
TATTTTAGAGACACAAATATTTAGTTCGCTTCATTTGAACAAATCGGCGAAA
ATTGGCTAGCTCGCCAAACTTTCTGTAACCAAGGACAATGGTTTTATTTTAAA
CCATTAAAACTTTAGACCCACTAGCTCCTAGATCCCCCTCAAAGATTTAAA
AAAAAAAAAACACGATACCCATTTCTACTGAACTTCGTTTTTGCTTGTCGTTTT
TTCCACTCGAACGGAAATGAGCTGACAGCGCACCGCACACGTCGATTGCAGA
AAACATCGGATAAAACAGGAGGAAAAGTTGTGCAAGGTGGAAAAGTGTGTT
TACCAACTATTGTTAGAGGCGTTCAAAGAATTACGCAGCTTTCCGTTAGTTA
GCAAGGGGTCACCGGGGAGCGTTACGTTTGCATTGCGTATTTCCGCTAAATGT

FIGURE 17 (Continued)

CATCGGAAAAGGCAAACGGCGAAATGCGAAACGAAAGTTTTTTGATTGCCCG
TGTTAATCGATATCGATGCACAACTATTTGCATTGCAACCGTTGCAAGAATA
TGCAAGAAGTTGGGGGCGGCCGCGGCAGGGGGTGGAAGTTGAGTGCGTAAG
TTGGCTAAAGCGGAAACAGGAAATGAGAAAATTTTGCAGAGCAAACCCCGA
ACTGGAAATGCAACTAACTGGGCACATGCACTTTGCGAAATCATTGGATAGC
GTTAAGAAATTTATTTTAAAATTGTAACAACTTTAATCGTATTCAAAGCA
ATTAAATCCCAATCCAATTCTTATATAAAATCCTTACAAGATTATTCTATTTA
CTGTAAATCTAAGCAAAAACCTCCCTTTGCAAAATATTTCGCTGCACAGCACA
GATCAGTGAAATAATCAAATGAAGTCTTGAAATAACGAAAAACCCCAATTG
CGTGTGGAAC TGCCCCAATGCTTTTGCTTCGGTTTCGTACCTGGCCGTGGTG
CAGTCCCTGTAGAGGATGTCGAAGTCCTTGACGACAGCAACTTGACGCGAT
TGACGCCCGGCTGGATGGCGCCCAAGCCGCGTAATATGCGCACCTGTTCCAC
ATTGCAGACGAGCGGTACGATGTCAAGGCGCTTTAGTTTGGTATAAACCGTA
TGCAGACCGCCGACCAAGTGCTTCAGGAAGAGCTCGAAGGCCTGCGGCAGGC
AGAGCATCGTTTCGTTGCTAATTATGAATGCGGCGACCTTCTGACCCCGGTAC
TCCACCAGCTTGCACTCATTGGCACTGGGATCCGAGGTGGAGATCGGCGGGCG
GTGAGTTGTACGACCTTGGCGGCACATGGTGATGGGCGGCGGCCATCAGTTC
CAAGGGGGAGGCATGGTGCATCATCTGCAGGGAGTTGAGGAGCCCCAGCGA
ATGGGGCGGCAGTCCATGGGGCATTCTGGGCGGTAGGCCCGTCGGCAGTCCG
TTGCCCGATGGCATTCCATGTGGCGGGGGGCTGAGCTGATGGTGTTGCTGCTG
CTGCTGTTGCTGCTGCTGTTGTTGCTGCTGTTGCTGCATCTGCTGCATCATGGA
GTGGTTGAGGGAGCTCACCGGACTGACGGCACTGGGATGGCGACTTGTTGAA
CTGGCCGGTGAGCAACTGGATCCTCGTCCTGTGTGCGAGCTCCGTCCATTTGG
ACGATCCTCGTTGGCTCCACGCGAACTGTTGCTACCGTCGCGTCCATTGTGCT
GCTGCTGTTGCTGCTGGGCTGCTGCGGCTGCCGCTGCTGCGGCTGCCTGCTGC
TGCTGCTGGTGATGCATCAACATGGCGGTGGTGTTTCATATTGCCCGCGGCTCT
TTCAATACCACTATTAATATTGTTATTTATTGCGCCCGCTTTATTGTTGTTATT
TTCACTCTGTTCACTTGTCACAGAATCCATACTTCATCATGGCCGACACTTTTG
TTTATTTACTTTTTAATCGATTCTGTTAATTTGACGTTTTTTCTATCGTGACAAA
AATTTGACACAAAGTAAGGGAGAAATAGAAAATAGATGGTGAGAGGAAGAT
AAATAATTAATGAACCTCTTAATTCATTTTTTAATTATTTATTAGGCTTCTATATG
CAAATTCTAAGTGAGCGTGTCTCGTATATTCCCTATCCGCTTATTATTGGCTTTA
CATTTTTAATACTTCTGTAAGTTTTATAACATCAAATTTAAATGCAGACCTTC
AAAAAATTTACAAACGATTTAGGATTTGTATTAGGCTCAGCTATGCTCCTATT
TATTAATAATCTATTTTTGAGCCAGTTTAGTTAGTTATATGGTAGCTACAAGTT
TATATTGCTAAATATTTTTTGTAATTAATATCCTAACAAACATTTTACTTACA
AAGAAATATAGAGAACTAACAGAAAATAGAAAAGTTTCCTTTCAGACATTTA
AAGTCCGATTATCTTCTAATACCCCCCATAAATAATCCTTTATCAACAGAACT
ATTGCTTTGCAAACCTTTGCTTTAATTAAGTTTTGGGAAAAACAAGGCAATGAA
GCTAATTTGGATCCTTACTGCCAATTTGCATAAATATACCTATTGTCAGCTTT
ATTTGAATAATTCGATATAGAACATAGATTTACCTTTAAGGAGGTCTAAAAGT
AATTTATAAACTCAACATCACTGACACAAGACACTCGCGCACTTTGCTTTTTTG
AATTTGCTGTGAAATATATACTCTGAATATTTCAAGTTATTTATCCGATTGC
CCGCTTGTTAATCGAGTTTGAATAACCGTTTTTCGTAAGTGAATTTTGGA
CCGGAGCTGTGTCCGTTTTTCGAGTACCGTACCGACGGATTGTCACCTCAGAGAT
TGAGAGATGGCAGCTACTCCGCTGCGACGGCGACGGTGGCGTCGCTGCCTCT

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FIGURE 17 (Continued)

GCTTCTTCGCCTTCGACTGGTTCCTCTTCCCCCTCTCGTTCGGAGAAATCAAC
GAAACGAATTGCATTCGAATGGGAATCGACTGAGAGCGAGACGGCGCGAGG
CGACGACTGCGAGTGAGCGAGTGAGCGGGCGCTAACGAGTGCTATTTTTTTA
GCCCACCCACACACACGTACGTACGTACGTACACACGAAGCGCTACCGTTAT
GTACTGAGAGAAATGCGCGCGCAAAAGTTTTATTGCATTACCTTCTCTTGCGA
ATGACAAATTCGTAATGAAAGGCGAGTTTCAATTTCGATTCTTTTCGGATTTTC
GTGGCAGCGACGCCGGCAGCGCGGTCTGGCCGAGACGAGTGTGCTTGTATGTG
TGTGTCTGTGCCTGTGAGAGCGAGCTGGTGTATCTGTATCTGCGATTGTGCAA
AACCAGAATACGAATACGAGTACGAATACGAATGTCTGTTGCCCGTCCACGT
CTCGCATTACACCAATACCAGGCCAAAAAGGGGAGTGGTATGTGCGATTGAT
CGGTGTGTTTGCATCTGTGTATAATTTCTGTGTGCAACCCCGAAAAATACAATGA
CAAACGTAATCGCTCTCTCTCTCTTGCATTTCGTTTTATTTATTTTTTCAATTCGT
TTGTGCGTGTGTGTTCTTCAAATCCTCCCGCTCTCTCTCTTTGGAAAAAAA
ACGTTTTTCATTTCAATTTCAATTCGTTTCAGTCTGAGCCCTCTCTCTCACACC
ATCTCGCCATCTCTGTGCGACGCTCAGGTGGGCTGCAACCAATAAACACGAG
CGAGCGAGAAAGCAGCATATTTGCATAGCCAGTCGTACATGTTTGCCTCTC
GCTCGCCCCCATGGGCGACGCCTTATATAAAACAAATGACAATTGTTTTGGCAT
TTTGTGTTGCAAAGTAAATTATAATAAATGCATTGCCAGAGAAGAAAAGTAA
AAAAAAATAGCTTTACTTCGAGTTTTCGCGAGCTGTCTTTGACAAAAAGCATT
TAATTTCAATTAAAAGTAAATGACAAACTTTCAACGAATTATACTTTTCGGGG
CAGTGTGCTATCTCTTTCCGTCCCAAGCTTTGATTTTTTTTGTCAACCGTTTT
CCGTTTCCCATTCGTTTCCATTCGAGTCCCGTTTATTTGTATTTCTTTTTGTGT
GCTGATTTCGGAGGAGAGCAGCACTATGGCAGGGCATCTTTCTTCCACTTACA
CATATTGCGATAATGGGGTTTTTTTTTCGCCTGAGGGGCGTTTCGTTTTTCGGGT
CTTATAAATAGCATTGCTTATAAATTCTGGCATCGCACCTTTGCCACCTCTAT
ATGTTTATGTACAATGTATCTGAGAGCTCGGTCATTTTTCTATTATTTGTCTTC
GTTTCGCCTTCTGCGATTCTTCTCCATAACGATTGCCATTCCGTGCGCGAACC
AATCGCATTCCGTTCTCTCCATTTGAGAGTTCCATGTACATATTTCTTTCTATA
TGGAATGGAATACGTCTTTATGTATTGTGTTTGACATGACGTATGAATTTT
TCTTGTTTCGTTTCGTTTGGGGCTTTTCTTTTGTGGATTTCCTCACCCACTGTCTT
TTAGGTGACAGCAACCATTAAATATTAAATTGATTGCAAATGTGGATTTCCAA
CAGCTTTTAGAAAAATATTTTCGGGCTTTAAAGAAGAATTTAAAACACAATAA
TTATTGTAATGTAAATATTTTATTTTACATCGGTTTGTTTCATTAAAAAATAG
TTATAAGATTATATTAGATATGAAATTAATATGTAACGCTACTTTTTTTCTA
AACTGTGACATTTTAGGCTATTTTTTCTTTTACCATTTCCTTATGTCATATGAA
TTTCATTTAATTATGACATATACATGAATCGCTGGCTTTAAATTCGAATAAGT
ACATTAAATTTACCAAAAATGACATGCAGAATTA AAAAGTATTCATTCAAAC
AAATTTGTTTTTCCCCCATAAATGGACAACAAAAAGGTACTGCCTCTATCATC
CAAGTGTCAAATATGTCATAGCAACCAACTATCGTCAGTAAGAAATGAGTT
CTACAACATGCAACTTTTTTTCATGGTGTGCAACTGTGGGCGGGAAGTTTGATT
TTTCGCAACAAACAGCTCGCTTTGAACTCTGGTTTTTCTCTTTAATAAATGCA
ACTGATCTAACTATTAAGTAAAATTGTATTTTTTATTAACCACAAGCAAGCGC
AAAGATGAGTTTATATTCTAAAAAAAAGGAGGGTGATTAATTTCTATTAGTTT
GGATTACAAATTTGGACTAGGAGTCAATTTGAAAGTCGTTATATCAATAATA
CTTCTGGACTTTGAAGCGACAGTTACTGTTCCATAACTTCGGATTATCAGCTT
TGCCTTCACCACATATATAGAGTATTCTCTGGATGTGTCGAGATTGTATTTTT

FIGURE 17 (Continued)

AAACGACGACTGGATGGCAAAAGTTCAGTGCGCTCGCAGCTATTATGTGGAT
TATCTGCCTCTTGCTGGTGCCCTTGTGGCGGCCAGTTCCAATACAAGACTTC
TAAATGGCATCCTAAGTCATGTGGACAAGGAAGCCAATCCCTGTGAGAACTA
CTACAACCACGCCTGCGGCCAGTACAACATGCGTCACATCGACGACACCTTC
TTCGACATTATACAAATGCTGGATCACCAGGTAAACCAGAACTTGGTGAAAC
TAATGGACGAGCTGGAAATGAGTTCTCAATTGCCGGACTTTAATGTATCTAGT
GTAGATGGCAAGGTCCTTCGTTACTACCTTAGTTGTCGTGGAGCGCCGCGGA
ATATGGATAGTTTAAGCCAGTATCTGAAAGTGATTTCGCCCGGCGAAGGACT
CACATGGCCTCAATTTCATTCCGGACGGTAGTTCTTGGCCCCAGGAGAATTTCA
AATGGCTCAAGGCACTGGCTCATCTGCATCGCTACGGTCTAACTAACGTGTTT
TTTAACCTTGAAGTCGTGTCAAACCCACGAAATGCCAGCGAGTACATGGTAG
AATTAAATACACCCACTTTTGGAGAAGAATCTCAACTGCCGAACAGTTTTATT
GAAATTCTATCCGTTCTCTATATCATAAAGGTCCTTCCAGTGAAATCATTAC
TCTGGCGCGAAAAATGCGAACGCTTGAATTGTTGCTTAAACGATGATCAAT
CCGATCGACACACTGAATAATAGATACATTAGTATCCGCGATTTTCAGATGG
AAACCGGTCACAACTGGCAGCGTTTCTTTGAGATTTAATAGGCTCCAGCGCA
GCCCCAGAACTCCAAGTGTTGGTGCGCAATTTTAGGTACTTTACCGCCCTTAA
GGAATAATGGACAAACAGGATGCTCGGCTGGTGGCCAGCTACATAATGACC
CGATTTGCAATATTTCTATTGGATGAAACCATGGGTGGCAGAGAATCCACGG
AGTGTGTGTACAGGTGCGCCGCAACATGAATTTGGCTGCAAACATGCTCTA
TAAGGAACGATTTTTTCGAAGACTCCACTTTTCAGTGCCAATATCCTGGAAATTA
AGGACATTTTCGAGAACTACGCCATCAGTTTCTGCTGCAAGTCGATCAAAA
TCATCTAGAGTTGACTGCTTTGCAGATGAAATTTTTTCGTTCGAAAGGCAGAGG
CAATTGAGATCAACGTTGTGAATCTTCCAAAAACCGATGATCTTCGCCATTTT
ATCGGCCAGTACTACCAAGACTTGCAGTTTCCCACTGGCGAGCTGGATTACC
ATCAGGAGCACCTCAAGGTGCTGCAGTTTCGCACCCAAAAGATGTTGGCCCA
ATCCAGCAAAGGGCACTCAGAGGAGCAGAATATTTTGACTTACAGGAGCCAA
GCGGCGCCATTGCCTCCACCTCGTACTATGTGATGCGCCCCAATGTGATTATT
GTCCCCCTTGGGCTACTGCAAGAGCCATTCTTTCAGCTGGAAAGCGAAGATG
TCTTCAAATACAGCCTGATGGGATATATTATGGCACATCACTTGATAAGCGCC
TTTGCCACCGAGGGCATTACAATTGGCAGCGATGGAAACGATCAATCATTTA
GATCGCATCGTTTTGAAGAAGCAGTCAGTTGCTTGTACGCAATTCAGAGAA
CATCGATGAAAGCATGGGCGATATTGCTGGTTTAGAACTGGCCTATTTTACTT
ATGCTAAGATGGCCAAGAATCGAAACCGTTTGGATTTCACCCATTTGCCACC
GGAGCAGATATTCTTCCTAAATGTTGGCCAGTTCTTCTGCGGCAATAGCGATA
TGTTGGTTCAGTACAAGGAAGATCAAGTGCGTTTACAGCGAGCTATTGAAGG
GTTTGAGCCATTTGACAAGGCTTTTGGGTGCTACCGCAATAAGCCTAAGCAC
GAGAAGTGTGCTTTATAGTGAATACCTTGTACATATGCTTAGAAATACATATT
TTTTGATAACAATAATACAAGACAATCGTGTTAAATTATAAAAGTGTTACAAT
CACATCCATTCTGTTCTTTTAAAATTAGTTTTTAAACTAACAATAGTCAATAGG
CTAAGATAGTTAAATGATCATCATTCGAATAAACAACGTTCAAGATTGACTCT
TCAATGTCATGCACCTGCAAGATTACCATTTATTATAAATTAAAAAACACAC
AAAGTTATACGTGTGTTACTTACATGCATTACATTCGGGCCTGGCCATCCACT
TAATATACTGAGATGTAGCGGTCTTTGATTTGCGGGATCTCTTATGGATTTTA
GAACATTGTAACTTTGCTGACAAAGTAAATTCAACTTTTAACGACTTGTGGT
GTGTGCGGCCCGATGAAATGTCTTAAAATACAAATTAAATACAATTCAATA

FIGURE 17 (Continued)

TAATTCAGACGTCAAAAGGTTTAAAGTTAAAATATATTTTACCTTTTAGTGTT
ATTTATACGTATGAGCCTTGAAAACACAGTTGAATATCAAACGGATTTTGTGTT
ACCAACAGATTCCAACAGATTCTCCAACCTTTCGTTTTTTGATTGCCTATTCACT
CGAAGATCTATTTCCAGTACTATGATCCTCCATAGTAGAGTCAGCTCAGGATC
TTGTGATAATCCGCAAGCAATTCGACAAAGAATTCGTCGGCCAGAACAAAAT
TTATTAAATCATTGTAGTCATTCTCAGGATCTCTCTTAACTGGCAATCCGTAA
TAACGTATTTTATTATCTCCAAAATACAGTCGGAATTCAGATTAAATTTGCCG
TTTCCGTCCTTTTTTATAAATATACATACAAATATACTAAGCAATAGACTGAA
ATGAATTCTAGAATTTGAGGAAACTAATTATGTACCTTTATGAATACTTTTCC
TACTTTGTACTAATCAAACCTAATTTTTAACAGATTTTTCATGCCGAATGATTA
CAATCTTATTTGGATGATTTGATAGAGCTTAGGAATAATGGTTTTAATTTTGG
ATTAAAGAGTTGCGATTAAGAAACGAAGATATTATCTAGTTTTTTGAAGAACA
CAGGGTACTTTAAATTTTCGCACGCGGAACGTCAAAACAAGAAGAAGTTTTCA
TCAACACTGAATTTCCGCTTGGTAATCAGCTGATAAGCGTGCTCACGATAGCC
GAGTTCACATCCAACAGATGTTTCCCTTAGCAGGGTTTCAGACCCAAATGATG
ATTTATCTTATTTTGATTAAGCTCCAACACGCATTGCTTTGCATAATTCAGGTA
TTATTAGGCTGCTTAATATACAATCCACTTATATTGTTGTGTCCATGAGGAAC
ATCGACACGTGAGGATAAAAAATATTTATTTATCGATATATTTTTACTCTTGAG
CCTTTTGCACACCCCTAGTTGTGTTCCA

FIGURE 18

dMLF 5' region, 8374 base pairs

GCCTGATTGTTTTCCACTTTGCAGCAGAGGAGCCGGGAAGGAGCGGTAGAGG
CGCACCCAGTGTATCCGGCAAAGGCAAGTCACCCAGGTGCGTTCCATGCCC
AGCTCTCCGCTGCCTCAGCGATCCGCTACGCCGACGCGGCTGATGAGCCAAC
GTGTCCGTGAGGCGGCCGAGCGTCTTGCCCAACAGCACACGGTGGCCAGTGC
TCAGCGGCATTTGGGCAATGGGAGAGGCACTGGCACTGGCAATGGAAATGGC
AATAGCAATAGTAATGGCAATGGTAATGGGAACACCGCGGAGACGAATCGC
GAATCACGCGCGCGACGTCTCATCAACCGATTCAATAGCGAAACGCAGCATA
TCACGTCCTAGTTTAAGTCGGTTAAATGCCGACGAGCATAACTTTATTACAGA
TAAAGCAGATATAGCATTGTTTAAAGTAAAAAATATATATATATACCCAGAG
AACTTTACGAAACACTCGAATATGAATGCGACTGCGGATCAGCATCCCACC
CACCCACACACACACGTCTACCCACTCACAGTAGGATATATGTATGTATGTCT
GCATTCAAGCGGATGCACTCCCTCCGTTTCAGAGGGAAGTGTACTTAGGCTAG
AGGAAGCTAAGTGTTTAAATTATTGTATCGATTTATATACATATTTACCATAC
TAATTAAAGTTAATGTAACGAAAACGCAGGATCAGTAATCTTATTTAGTTCA
ATGGTAATCAATGTGCGATTAGCGGATGATCGCGCTCCTTGAGTCGCACCCA
CAGTCCGCCGGAGGCTCTCAGCGTAATCCGGAAGGTGGCCGCAATGGTTGTC
TTTCCGGTTACAGGAAGCAGCTGGTAGCTACGCAGCAGGCGCGACACTATGG
TCTTGATCTCCATGATGGCGAATCGATTGCCAATGCAATATCTCGGTCCAGCG
CTGAAGGGTAAAAAGGCGTAGGGATGACGGTTCTCGGAGTTCTCGGGCGAAA
ATCGCTCCGGCTGGAACCTTTTCCGGATCGGGATAAATGTGGGCAAGACGATG
GGTGGCATAGGGGCAAATGAAAACGTTGCTGCCGGCGGGCAATGTGTGCTTT
GCCAGGCGAACCTCTTCGCCCAGTTTACGAGCAATAAGCGGGACACTGGGAT
ACAGACGCAGTGCCTCCTTGATGCACATCTCCATGTAACGCATCTCGTGCAGA
TCCGTCATCGTGGGAGCTCTATTACTGTCCTCGAATATGGTCGCCAGCTCCAG
GACACAGCGATCCTGGCACTCGGGATTCTGTGTCAGCAGAAAGAGAGTGAAG
GCCACGGCGGCACCCACCGAATCCTGGCCAGCCAGCATAAAGGTACAGGCCT
CGTTGACGATATCCTCCTCGGTGAAGTCCCGATTGCTCTCGGAGATCTCGATC
ATGTGGTTCGAGCAGACACTTTCGCTCGCTATTGCCATTATTATTGTTCTGGAT
TTGGCGACGTCTCTGGATCATTTTTCGTGTGAAGTCATTGAGGCGCTTCTTCT
GGTTAAGCTCATCGTTGGCCATCTTGGTCCAGTGGTAGATCCCGTCCAGCAGC
AGCCAGGGTTGCGTAAACCGCGCGGGCATCATGATCTTGCCCTGGCGGAACG
GCGAGTCCTCCATCATGGCCACATCCTGACCTCTTTTCTTGATCGGCACACCC
AAAACGGCCTCTGCAAGTCGTTTCAGGGATTAAGTGAGAAATTATAGCTTGCT
AATCCCCTAGAGACTCACCATTTAGTATGTCCAGTACACAGTTGTTACGTAC
TTGGCAATATTTATCTCCGTTCCACGGCTTCGGCATCCAGATTCTCGTACAA
CGATTGCGAGGCATCCACAAAGGTGTCGATGAACTTCTCCAGCAGATTGTGA
TGAAACGCTGGCTGGATGAGCCGTCGATGATTGCTCCACTTGGAACCACTGC
TGGTTATCAGCCCATCACCCAGGAAATTGTGCATCAGTCGGTAGAAGAAGAC
CTTGTTGGTGTGCTTCTTCGAGGAGAGTATCACCTGCAGATCCTCCGGCTCCA
GGACAGCAAAGAAGGGAAAGAGCAGCACCCAGATCCGCACCAGAGATCCAT
ATAGATCGAAGGCCTTGCCGGCACATCTGCGCATCACTGTGAAATGGGATTC
AATTTAACTTAAAAGGTATCTTTCACGAAAAGGTTTCTTCAAGGATCTTACAG

[illegible]

TCCTTATCCGTGACCAGCATGCAGTTGCCAGAAATGGCAGCGATGGCGGAC
CCGTGAGTCTCAGCGAGAGGAGAACCGATCTCAAGTACGTGTTCAGGGTGGC
GTAGAATGTGTAGATGCTCAGGCTGATCACCAGGAGGATCAGAATGGAGCAT
AGCTCCAAATTGGTGGTGCGCTCCAGCTGTGGGGGCGAAAGCAAACGTAAAT
GCATTGGGTCAAGTCGCGTGGATAATTGCCCGCTTAGGTCAATATTTGGTTTG
CTATCGAGAACGCCGAGCTCTTGAACGCACTTCATCAGCTACGCACTGCGCTC
ACTGGAGTCTAATTAAGTGAAGGAATCTTGGAGCACTTAGGCATTTCGAACCTG
GATGCGAGCACTTGCCCTTGCCGCGTGTGCAAGTTTTCGGCAAACACACGTT
ATCGTAATCGCAACGAAAGTATAAGTTATGTATCTAACTGCGGTGTGAATTG
CTTGGGCCAACATGGCGTATGGGCGATGCTATAAGTACGTGTGTGTGTATCC
ATAAGATCGATTAAAGCACCACACCGTTCATGTGTACGTGTTGCTTTGCTTTG
GTTTTTTTTTCTTTATTTTTGGGCCATTTCGCGTCGATGTTTCGTGGTGCAACAG
GTTACACGATGAGCACAAAACATGACAAATGATGATGATCACCGGACAAAA
ATCCAGGGACAGCCTTTTGTGTTGCCCACTTCCCACACCTGTCGTGCGCCAC
ACCCTTGCACTTAACCCCCCCCCCCCCCCCCCAAAAAAAAAACCCCTTTGTTTG
GTTCTGGACGAGAGTGAGAGCCCCAACACCATTAGCCAAATGCGATTGGTTT
CAGGGCCAAGTGAAACCACCGGTTGGTTAACTGACTCAGATCTCAATGATTA
ATTTATTACGGACAAGGAATCGGCAAACGATCGCAGTTGGTCATCATAAAGT
TTATCCAAAAATCTAGGTGGCATTCCATTTAGTGGGAACTTCTTACCATCAGT
TCGTAGTAAGCTAAGTTAAAGAGTAAAATAATAGGCGCTTTTAATCCTCCTCA
GCCACCTCATCCTCGTAGCCCTCGGGCAGGGCATTACCTCGGCATTGTGAAA
CAAACCTGCGATTGCCATCTCCCCATGGGAATCGTTTGGTCCGCCGCTCAGGT
ACTCGTACTTGGCGAACGGCTCCCGCTCCACGTGCTTGTGTCCGGTGAAGGCG
TTTGCGGCGCACAGGACGATGGCCGGTAGGGCCAGCAGGAAGGTGACACGC
TCCACAGACCAGCGGTATTGGCGGGCATATTGCCATAAGCCGGATATCAA
AGATCGGCATGTATCTGCACAATAACTCGACTTATTCTGATGCCTGGCTGGAT
GGCTAAGCTAGCTTGAATTTGAATACTACGTACTGTAGCGATTTGAATCTGAT
CCGTAACACCCACGCCTGCTGCCCCGAACTATTGTCGCAATTAGGAACTCTCA
AGGGGATCCGAGCCAGCGCCACAAGGTCCAACAACCCGCGTATCTTTGTTTA
ATCAGCCCAATATTTGACCAGAAACCGCTGAAGCGTCCAGAAGGCTTGCGCT
CCGCTCCAAGCGGCTACTTCTATTTTTTTTTTCTCTTCATCGAATATTTCTTTCTT
AGTTTCGAATGCTTCTTTTTTTTTTTTGGGCACGGCATATCCATCCCCATCCAGG
CTGCGAGGTGTGCAGAACCCGCGCCGCTGTTTGCTCGCCAATTGGCACCTGGC
CACTAATAGATATACATCATGATTATTTCCCACTAATTCCATAAGTTATCATA
ATGGTCTTCTTAAACGAGAGGCTGCTTGTGAGGGCACTAAGACCGCCCCAAAA
TCTAACGATCCATTGAGATTGCGGTAAAAATGATTCAAATGCAAGCGAAGT
TACTAAAATTTGTGAGAGTATATCTAGTTGAAAACCTGAACTTGAAAATGTG
GTTTTCATAAAATTATCCAAATTGATGGGTGTGAATTAATAATTAAATTAATA
CTTGCACTTGAATACTCAAATTCATTGCTCAATTCAATTGATAGATAAATGAT
GATTAATAATAAGTTATAAACCTAGATCATTTCACTTTAGTATTGGTAATGA
AATTTAGGTTTATATATCCTCACTCTTCTTAAAGTAATGTAAATATTTGTTATC
CTTTAGGAAATACACCTTATTAAATAAATTATTTTAAATTCTATTAAAATTCTT
TAAAAAACAGAAACGTAATAGCCACCATTTTACATTTTACTTAAACGTTTTT
CCTTTTCTTTTTTAAACTTTAGCTGTGAGTAATCCTTTTTATTTCATAACGAATT
GCGTTTAAATATTTTTATATTTTCTTCACTCACCACCTTTTTCCACAAACATTTT
AGTCACGTATTTGTATTCCCTTGATATAGTCAATATATTTTGTTTTTATCTTTA

[illegible]

[illegible][illegible]